

# SCORE Search Results Details for Application 10552515 and Search Result 20080624\_083148\_us-10-552-515-1.rup.

<a href="#">Score Home</a>	<a href="#">Retrieve Application</a>	<a href="#">SCORE System</a>	<a href="#">SCORE</a>	<a href="#">Comments /</a>
<a href="#">Page</a>	<a href="#">List</a>	<a href="#">Overview</a>	<a href="#">FAQ</a>	<a href="#">Suggestions</a>

This page gives you Search Results detail for the Application 10552515 and Search Result 20080624\_083148\_us-10-552-515-1.rup.

[Go Back to previous page](#)

GenCore version 6.2.1  
Copyright (c) 1993 - 2008 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 24, 2008, 08:32:16 ; Search time 518 Seconds  
(without alignments)  
2963.070 Million cell updates/sec

Title: US-10-552-515-1  
Perfect score: 4950  
Sequence: 1 MRMAATAWAGLQGPPLPTLC.....SELSSHWTPFTVPKASQLQQ 933

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 5032670 seqs, 1645091341 residues

Total number of hits satisfying chosen parameters: 5032670

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_12.1:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	4950	100.0	933	1 TM16G_HUMAN	Q6iwh7 homo sapien
2	3771.5	76.2	859	1 TM16G_MOUSE	Q14at5 mus musculu

3	3764	76.0	860	1	TM16G_RAT	Q6ift6	rattus norv
4	1539.5	31.1	920	2	A6QLE6_BOVIN	A6qle6	bos taurus
5	1525.5	30.8	903	2	Q1AP36_STRPU	Q1ap36	strongyloce
6	1525.5	30.8	955	1	TM16D_HUMAN	Q32m45	homo sapien
7	1523	30.8	921	2	Q1AP35_STRPU	Q1ap35	strongyloce
8	1512.5	30.6	981	2	A2AHE5_MOUSE	A2ahe5	mus musculu
9	1504	30.4	981	1	TM16C_HUMAN	Q9byt9	homo sapien
10	1500.5	30.3	900	2	A1A5Z4_DANRE	A1a5z4	danio rerio
11	1497	30.2	921	2	Q1AP37_STRPU	Q1ap37	strongyloce
12	1489	30.1	960	1	TM16A_MOUSE	Q8bhy3	mus musculu
13	1482	29.9	986	1	TM16A_HUMAN	Q5xxa6	homo sapien
14	1467.5	29.6	913	2	Q8CFW1_MOUSE	Q8cfw1	mus musculu
15	1464	29.6	999	1	TM16B_HUMAN	Q9nq90	homo sapien
16	1455	29.4	913	1	TM16E_HUMAN	Q75v66	homo sapien
17	1449	29.3	896	2	Q6DDQ3_XENLA	Q6ddq3	xenopus lae
18	1448.5	29.3	1014	2	Q175J3_AEDAE	Q175j3	aedes aegyp
19	1445	29.2	1219	2	Q9VTS0_DROME	Q9vts0	drosophila
20	1443	29.2	1235	2	Q2M0Y5_DROPS	Q2m0y5	drosophila
21	1438.5	29.1	1117	2	Q0IEX5_AEDAE	Q0iex5	aedes aegyp
22	1433	28.9	906	2	Q7QDY0_ANOGA	Q7qdy0	anopheles g
23	1402.5	28.3	910	1	TM16F_HUMAN	Q4kmq2	homo sapien
24	1402	28.3	904	1	TM16E_MOUSE	Q75ur0	mus musculu
25	1402	28.3	904	2	Q3V657_MOUSE	Q3v657	mus musculu
26	1389	28.1	909	2	A6NNM6_HUMAN	A6nnm6	homo sapien
27	1384	28.0	1613	2	Q4S1F6_TETNG	Q4s1f6	tetraodon n
28	1383.5	27.9	871	2	Q8JFT1_DANRE	Q8jft1	danio rerio
29	1382.5	27.9	412	2	Q4SC97_TETNG	Q4sc97	tetraodon n
30	1371	27.7	911	1	TM16F_MOUSE	Q6p9j9	mus musculu
31	1369.5	27.7	1075	2	Q9VDV4_DROME	Q9vdv4	drosophila
32	1367.5	27.6	712	2	Q8NCT7_HUMAN	Q8nct7	homo sapien
33	1367.5	27.6	926	2	Q8IN71_DROME	Q8in71	drosophila
34	1366.5	27.6	972	2	Q86P24_DROME	Q86p24	drosophila
35	1354	27.4	1062	2	Q293M2_DROPS	Q293m2	drosophila
36	1333	26.9	895	2	Q16L02_AEDAE	Q16l02	aedes aegyp
37	1319	26.6	1035	2	Q4SSV5_TETNG	Q4ssv5	tetraodon n
38	1306	26.4	863	2	Q16MH2_AEDAE	Q16mh2	aedes aegyp
39	1290	26.1	823	2	Q7QEP9_ANOGA	Q7qep9	anopheles g
40	1269	25.6	1017	2	Q29H97_DROPS	Q29h97	drosophila
41	1254.5	25.3	854	2	Q2VPA8_MOUSE	Q2vpa8	mus musculu
42	1249	25.2	984	2	Q8MT62_DROME	Q8mt62	drosophila
43	1237.5	25.0	971	2	Q4REV7_TETNG	Q4rev7	tetraodon n
44	1199.5	24.2	1043	2	Q9VYS8_DROME	Q9vys8	drosophila
45	1199.5	24.2	1059	2	Q76NS2_DROME	Q76ns2	drosophila

## ALIGNMENTS

## RESULT 1

TM16G\_HUMAN

ID TM16G\_HUMAN Reviewed; 933 AA.

AC Q6IWH7; Q6IWH6;

DT 29-MAY-2007, integrated into UniProtKB/Swiss-Prot.

DT 05-JUL-2004, sequence version 1.

DT 24-JUL-2007, entry version 21.

DE Transmembrane protein 16G (New gene expressed in prostate) (Prostate

DE cancer-associated protein 5) (IPCA-5) (Dresden-transmembrane protein  
DE of the prostate) (D-TMPP).

GN Name=TMEM16G; Synonyms=NGEP, PCANAP5;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
OC Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2), TISSUE SPECIFICITY,  
RP SUBCELLULAR LOCATION, AND TOPOLOGY.

RX PubMed=14981236; DOI=10.1073/pnas.0308746101;

RA Bera T.K., Das S., Maeda H., Beers R., Wolfgang C.D., Kumar V.,  
RA Hahn Y., Lee B., Pastan I.;

RT "NGEP, a gene encoding a membrane protein detected only in prostate  
RT cancer and normal prostate.";

RL Proc. Natl. Acad. Sci. U.S.A. 101:3059-3064(2004).

RN [2]

RP IDENTIFICATION.

RX PubMed=10613842; DOI=10.1101/gr.9.12.1198;

RA Walker M.G., Volkmuth W., Sprinzak E., Hodgson D., Klingler T.;

RT "Prediction of gene function by genome-scale expression analysis:  
RT prostate cancer-associated genes.";

RL Genome Res. 9:1198-1203(1999).

RN [3]

RP IDENTIFICATION.

RX PubMed=15375614;

RA Katoh M., Katoh M.;

RT "Characterization of human TMEM16G gene in silico.";

RL Int. J. Mol. Med. 14:759-764(2004).

RN [4]

RP ALTERNATIVE SPLICING (ISOFORM 3), TISSUE SPECIFICITY, AND INDUCTION BY  
RP ANDROGEN.

RX PubMed=15761874; DOI=10.1002/pros.20250;

RA Kiessling A., Weigle B., Fuessel S., Ebner R., Meye A., Rieger M.A.,  
RA Schmitz M., Temme A., Bachmann M., Wirth M.P., Rieber E.P.;

RT "D-TMPP: a novel androgen-regulated gene preferentially expressed in  
RT prostate and prostate cancer that is the first characterized member of  
RT an eukaryotic gene family.";

RL Prostate 64:387-400(2005).

RN [5]

RP FUNCTION, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.

RX PubMed=17308099; DOI=10.1158/0008-5472.CAN-06-2673;

RA Das S., Hahn Y., Nagata S., Willingham M.C., Bera T.K., Lee B.,  
RA Pastan I.;

RT "NGEP, a prostate-specific plasma membrane protein that promotes the  
RT association of LNCaP cells.";

RL Cancer Res. 67:1594-1601(2007).

CC -!- FUNCTION: May play a role in cell-cell interactions.

CC -!- SUBCELLULAR LOCATION: Isoform 1: Cell membrane; Multi-pass  
CC membrane protein. Isoform 2: Cytoplasm, cytosol. Note=Isoform 1  
CC concentrates at sites of cell-cell contact.

CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=3;

CC Name=1; Synonyms=NGEP-L;

```

CC      IsoId=Q6IWH7-1; Sequence=Displayed;
CC      Name=2; Synonyms=NGEP-S;
CC      IsoId=Q6IWH7-2; Sequence=VSP_026004, VSP_026005, VSP_026006;
CC      Name=3; Synonyms=D-TMPP;
CC      IsoId=Q6IWH7-3; Sequence=VSP_026004, VSP_026007, VSP_026008;
CC      !- TISSUE SPECIFICITY: Specifically expressed in epithelial cells of
CC      the prostate (at protein level).
CC      !- INDUCTION: Up-regulated by androgen.
CC      !- SIMILARITY: Belongs to the TMEM16 family.
CC      !- CAUTION: It is uncertain whether Met-1 or Met-55 is the initiator.
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NoDerivs License
CC      -----
DR      EMBL; AY617079; AAT40139.1; -; mRNA.
DR      EMBL; AY617080; AAT40140.1; -; mRNA.
DR      UniGene; Hs.163909; -.
DR      Ensembl; ENSG00000146205; Homo sapiens.
DR      HGNC; HGNC:31677; TMEM16G.
DR      MIM; 605096; gene.
DR      PharmGKB; PA32980; -.
DR      ArrayExpress; Q6IWH7; -.
DR      GO; GO:0005886; C:plasma membrane; IDA:MGI.
DR      InterPro; IPR007632; DUF590.
DR      PANTHER; PTHR12308; DUF590; 1.
DR      Pfam; PF04547; DUF590; 1.
PE      1: Evidence at protein level;
KW      Alternative splicing; Cytoplasm; Membrane; Polymorphism;
KW      Transmembrane.
FT      CHAIN          1      933      Transmembrane protein 16G.
FT                                     /FTId=PRO_0000289326.
FT      TOPO_DOM       1      355      Extracellular (Potential).
FT      TRANSMEM       356     376      Potential.
FT      TOPO_DOM       377     420      Cytoplasmic (Potential).
FT      TRANSMEM       421     441      Potential.
FT      TOPO_DOM       442     499      Extracellular (Potential).
FT      TRANSMEM       500     520      Potential.
FT      TOPO_DOM       521     550      Cytoplasmic (Potential).
FT      TRANSMEM       551     571      Potential.
FT      TOPO_DOM       572     588      Extracellular (Potential).
FT      TRANSMEM       589     609      Potential.
FT      TOPO_DOM       610     714      Cytoplasmic (Potential).
FT      TRANSMEM       715     735      Potential.
FT      TOPO_DOM       736     763      Extracellular (Potential).
FT      TRANSMEM       764     784      Potential.
FT      TOPO_DOM       785     843      Cytoplasmic (Potential).
FT      TRANSMEM       844     864      Potential.
FT      TOPO_DOM       865     933      Extracellular (Potential).
FT      VAR_SEQ        110     110      Missing (in isoform 2 and isoform 3).
FT                                     /FTId=VSP_026004.
FT      VAR_SEQ        158     180      QDVQDGNNTTVHYALLSASWAVLC -> VRGGCHGQGPRPCI
FT      HSVTHDLAA (in isoform 2).
FT      /FTId=VSP_026005.
FT      VAR_SEQ        181     933      Missing (in isoform 2).
FT      /FTId=VSP_026006.
FT      VAR_SEQ        859     859      H -> VAEAPAGSPIHGMRPRPCALPNSSTW (in

```

```
Query Match      100.0%;  Score 4950;  DB 1;  Length 933;
Best Local Similarity 100.0%;  Pred. No. 0;
Matches 933;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
```

http://es/ScoreAccessWeb/GetItem.action?AppId=105525...24\_083148\_us-10-552-515-1.rup&ItemType=4&startByte=0 (5 of 41)10/10/2008 8:48:54 AM

Qy	661	LIPKLKGWWQKFRLRSKKRKAGASAGASQGPWEDDYELVPCEGLFDEYLEMVLQFGFVTI	720
Db	661	LIPKLKGWWQKFRLRSKKRKAGASAGASQGPWEDDYELVPCEGLFDEYLEMVLQFGFVTI	720
Qy	721	FVAACPLAPLFPALLNNWVEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISN	780
Db	721	FVAACPLAPLFPALLNNWVEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISN	780
Qy	781	AFLALFSSDFLPRAYYRWTRAHDLRGFLNFTLARAPSSFAAAHNRTCERYAFRDDDGHYS	840
Db	781	AFLALFSSDFLPRAYYRWTRAHDLRGFLNFTLARAPSSFAAAHNRTCERYAFRDDDGHYS	840
Qy	841	QTYWNLLAIRLAFVIVFEHVFSVGRLDLLVPDIPESVEIKVKREYYLAKQALAENEVL	900
Db	841	QTYWNLLAIRLAFVIVFEHVFSVGRLDLLVPDIPESVEIKVKREYYLAKQALAENEVL	900
Qy	901	FGTNGTKDEQPKGSELSSHWPFTVPKASQLQQ	933
Db	901	FGTNGTKDEQPKGSELSSHWPFTVPKASQLQQ	933

RESULT 2

TM16G\_MOUSE

ID TM16G\_MOUSE Reviewed; 859 AA.

AC Q14AT5; Q6IFT5;

DT 29-MAY-2007, integrated into UniProtKB/Swiss-Prot.

DT 29-MAY-2007, sequence version 2.

DT 24-JUL-2007, entry version 9.

DE Transmembrane protein 16G (New gene expressed in prostate homolog).

GN Name=Tmem16g; Synonyms=Ngep;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muroidea; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=C57BL/6J;

RG The mouse genome sequencing consortium;

RL Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.

RN [2]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 2).

RX PubMed=15489334; DOI=10.1101/gr.2596504;

RG The MGC Project Team;

RT "The status, quality, and expansion of the NIH full-length cDNA

RT project: the Mammalian Gene Collection (MGC).";

RL Genome Res. 14:2121-2127(2004).

RN [3]

RP IDENTIFICATION.

RX PubMed=14981236; DOI=10.1073/pnas.0308746101;

RA Bera T.K., Das S., Maeda H., Beers R., Wolfgang C.D., Kumar V.,

RA Hahn Y., Lee B., Pastan I.;

RT "NGEP, a gene encoding a membrane protein detected only in prostate

RT cancer and normal prostate.";

RL Proc. Natl. Acad. Sci. U.S.A. 101:3059-3064(2004).

```

CC  -!- FUNCTION: May play a role in cell-cell interactions (By
CC      similarity).
CC  -!- SUBCELLULAR LOCATION: Cell membrane; Multi-pass membrane protein
CC      (By similarity). Note=Concentrates at sites of cell-cell contact
CC      (By similarity).
CC  -!- ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=2;
CC      Name=1;
CC      IsoId=Q14AT5-1; Sequence=Displayed;
CC      Name=2;
CC      IsoId=Q14AT5-2; Sequence=VSP_026009, VSP_026010;
CC  -!- SIMILARITY: Belongs to the TMEM16 family.
CC  -----
CC  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC  Distributed under the Creative Commons Attribution-NoDerivs License
CC  -----
DR  EMBL; AC108412; -; NOT_ANNOTATED_CDS; Genomic_DNA.
DR  EMBL; AC124669; -; NOT_ANNOTATED_CDS; Genomic_DNA.
DR  EMBL; BC116706; AAI16707.1; -; mRNA.
DR  EMBL; BK004075; DAA04566.1; -; mRNA.
DR  UniGene; Mm.297411; -.
DR  Ensembl; ENSMUSG00000034107; Mus musculus.
DR  MGI; MGI:3052714; Tmem16g.
DR  InterPro; IPR007632; DUF590.
DR  PANTHER; PTHR12308; DUF590; 1.
DR  Pfam; PF04547; DUF590; 1.
PE  2: Evidence at transcript level;
KW  Alternative splicing; Membrane; Transmembrane.
FT  CHAIN           1      859      Transmembrane protein 16G.
FT                                     /FTId=PRO_0000289327.
FT  TOPO_DOM        1      297      Extracellular (Potential).
FT  TRANSMEM        298     318      Potential.
FT  TOPO_DOM        319     362      Cytoplasmic (Potential).
FT  TRANSMEM        363     383      Potential.
FT  TOPO_DOM        384     441      Extracellular (Potential).
FT  TRANSMEM        442     462      Potential.
FT  TOPO_DOM        463     492      Cytoplasmic (Potential).
FT  TRANSMEM        493     513      Potential.
FT  TOPO_DOM        514     530      Extracellular (Potential).
FT  TRANSMEM        531     551      Potential.
FT  TOPO_DOM        552     651      Cytoplasmic (Potential).
FT  TRANSMEM        652     672      Potential.
FT  TOPO_DOM        673     700      Extracellular (Potential).
FT  TRANSMEM        701     721      Potential.
FT  TOPO_DOM        722     780      Cytoplasmic (Potential).
FT  TRANSMEM        781     801      Potential.
FT  TOPO_DOM        802     859      Extracellular (Potential).
FT  VAR_SEQ          836     843      ALLGATGV -> VTVGVTTGG (in isoform 2).
FT                                     /FTId=VSP_026009.
FT  VAR_SEQ          844     859      Missing (in isoform 2).
FT                                     /FTId=VSP_026010.
SQ  SEQUENCE        859 AA;  97128 MW;  82E1A473C59C8DA3 CRC64;

```

Query Match 76.2%; Score 3771.5; DB 1; Length 859;  
 Best Local Similarity 83.0%; Pred. No. 1e-300;

Matches	716;	Conservative	43;	Mismatches	95;	Indels	9;	Gaps	4;
Qy	55	MLRRRAQEEDSTVLIDVSPPEAEKRGSYGSTAHASEPGGQQAACRAGSPAKPRIADFLV	114	: :        :					
Db	1	MLRGQAREEDSVVLIDMASPEAGNGCSYGSTAQASEAGKQQVAPSRVGSSAKPPI-DFVL	59						
Qy	115	VWEEDLKLDRQQDSAARDRTDMHRTWRETFLDNLRAAGLCVDQQDVQDGNTTVHYALLSA	174	:  : :         :        :					
Db	60	VWEEDL---RNQENPTKDKTDTHEVWRETFLLENLCLAGLKIDQHDVQDEAAAVHYILLRA	116						
Qy	175	SWAVLCYYAEDLRLKLPLQELPNQASNWSAGLLAWLGIPNVLLEVPDVPPEYYSCRFRV	234	:             : :					
Db	117	PWAVLCYYAEDLRLKLPLQELPNQASNWSATLLEWLGI PNILLEHVPDTPPEYYSCQFKA	176						
Qy	235	NKLPRFLGSDNQDTFFTSTKRHQILFEILAKTPYGHEKKNLLGIHQLLAEGVLSAAFPLH	294	:					
Db	177	SKLQWFLGSDNQDTFFTSTKRHQILFEILAKTPYGHEKKGLFGIDQLLAEGVFSAAFPLH	236						
Qy	295	DGPFKTPPEGPQAPRLNQVLFQHWARWGKWNKYQPLDHVRRYFGEKVALYFAWLGFYT	354						
Db	237	DGPFSAVPESSQVLGLIQRQVLFQHWARWGKWNKYQPLDHVRRYFGEKVALYFAWLGFYT	296						
Qy	355	GWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPLCLDCPFWLLSSACALQA	414	:					
Db	297	GWLLPAAVVGTVVFLVGCFLVFSDIPTQELCHSSDSFDMCPLCSDCSFWLLSSACTLAQA	356						
Qy	415	GRLFDHGGTVFFSLFMALWAVLLEWYWKRSATLAYRWDCSDYEDTEERPRPQFAASAPM	474						
Db	357	GRLFDHGGTVFFSLFMALWAVLLEWYWKRNATLAYRWDCSDYEDIEERPRPQFAATAPM	416						
Qy	475	TAPNPITGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLVSIILYRAIMAIIVSRSGN	534	:         : :       :       :       :					
Db	417	TALNPITGEDEPYFPEKNRVRMLAGSVVLLMMVAVVIMCLVSVILYRAVMAIIVSRSDN	476						
Qy	535	TLAAWASRIASLTGSSVNLVFIILSKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIF	594	:					
Db	477	AFLSAWASRIASLTGSSVNLVFIILSKVYVLLAQVLTRWEMHRTQTEFEDAFTLKVFIF	536						
Qy	595	QFVNIFYSSPVYIAFFKGRFVGYPGNYHTLFGVRNEECAAGGCLIELAQELLVIMVGKQVI	654	:					
Db	537	QFVNIFYASPVYIAFFKGRFVGYPGNYHTLFGIRNEECPAGGCLSELAQELLVIMVGKQII	596						
Qy	655	NNMQEVLIPKLGWWQKFRRLRSKKRKAGASAGASQGPWEDDYELVPCEGLFDEYLEMVLQ	714	:     :              :           :					
Db	597	NNVQEVLPKLGKWCQKF---SRGKKAG--TGTHPAPWEADYELLPCEGLFHEYLEMVLQ	651						
Qy	715	FGFVTIFVAACPLAPLFA LLNNWVEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTH	774						
Db	652	FGFVTIFVAACPLAPLFA LLNNWVEIRLDARKFVCEYRRPVAERAQDIGIWFHILTGLTH	711						
Qy	775	LAVISNAFLLA FSSDFLPRAYYRWTRAHDLRGFLNFTLARAPSSFAAAHNRTCRIYAFRD	834						
Db	712	LAVISNAFLLA FSSDFLPRVYYSWTHAPDLHGFLNFTLARAPPTFTSAHNRTCRIYAFRD	771						
Qy	835	DDGHYSQTYWNLLAIRLAFVIVFEHVVSFVGRLLDLLVPDIPESVEIKVKREYYLAKQAL	894						



Db 772 DDGHYSPTYWTLLAIRLAFVIVFEHVVSIGRVLDLLVPDIPESVEIKVKREYYLAKQAL 831

Qy 895 AENEVLFGTNGTKDEQPKGSELS 917  
 |||| | | | ||:| | | |

Db 832 AENEALLGATGVKDDQPPSSEPS 854

RESULT 3

TM16G\_RAT

ID TM16G\_RAT Reviewed; 860 AA.

AC Q6IFT6;

DT 29-MAY-2007, integrated into UniProtKB/Swiss-Prot.

DT 05-JUL-2004, sequence version 1.

DT 24-JUL-2007, entry version 22.

DE Transmembrane protein 16G (New gene expressed in prostate homolog).

GN Name=Tmem16g; Synonyms=Ngep;

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muroidea; Muridae; Murinae; Rattus.

OX NCBI\_TaxID=10116;

RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=Brown Norway;

RX PubMed=15057822; DOI=10.1038/nature02426;

RA Gibbs R.A., Weinstock G.M., Metzker M.L., Muzny D.M., Sodergren E.J.,

RA Scherer S., Scott G., Steffen D., Worley K.C., Burch P.E., Okwuonu G.,

RA Hines S., Lewis L., Deramo C., Delgado O., Dugan-Rocha S., Miner G.,

RA Morgan M., Hawes A., Gill R., Holt R.A., Adams M.D., Amanatides P.G.,

RA Baden-Tillson H., Barnstead M., Chin S., Evans C.A., Ferriera S.,

RA Fosler C., Glodek A., Gu Z., Jennings D., Kraft C.L., Nguyen T.,

RA Pfannkoch C.M., Sitter C., Sutton G.G., Venter J.C., Woodage T.,

RA Smith D., Lee H.-M., Gustafson E., Cahill P., Kana A.,

RA Doucette-Stamm L., Weinstock K., Fechtel K., Weiss R.B., Dunn D.M.,

RA Green E.D., Blakesley R.W., Bouffard G.G., De Jong P.J., Osoegawa K.,

RA Zhu B., Marra M., Schein J., Bosdet I., Fjell C., Jones S.,

RA Krzywinski M., Mathewson C., Siddiqui A., Wye N., McPherson J.,

RA Zhao S., Fraser C.M., Shetty J., Shatsman S., Geer K., Chen Y.,

RA Abramzon S., Nierman W.C., Havlak P.H., Chen R., Durbin K.J., Egan A.,

RA Ren Y., Song X.-Z., Li B., Liu Y., Qin X., Cawley S., Cooney A.J.,

RA D'Souza L.M., Martin K., Wu J.Q., Gonzalez-Garay M.L., Jackson A.R.,

RA Kalafus K.J., McLeod M.P., Milosavljevic A., Virk D., Volkov A.,

RA Wheeler D.A., Zhang Z., Bailey J.A., Eichler E.E., Tuzun E.,

RA Birney E., Mongin E., Ureta-Vidal A., Woodwark C., Zdobnov E.,

RA Bork P., Suyama M., Torrents D., Alexandersson M., Trask B.J.,

RA Young J.M., Huang H., Wang H., Xing H., Daniels S., Gietzen D.,

RA Schmidt J., Stevens K., Vitt U., Wingrove J., Camara F., Mar Alba M.,

RA Abril J.F., Guigo R., Smit A., Dubchak I., Rubin E.M., Couronne O.,

RA Poliakov A., Huebner N., Ganten D., Goesele C., Hummel O.,

RA Kreitler T., Lee Y.-A., Monti J., Schulz H., Zimdahl H.,

RA Himmelbauer H., Lehrach H., Jacob H.J., Bromberg S.,

RA Gullings-Handley J., Jensen-Seaman M.I., Kwitek A.E., Lazar J.,

RA Pasko D., Tonellato P.J., Twigger S., Ponting C.P., Duarte J.M.,

RA Rice S., Goodstadt L., Beatson S.A., Emes R.D., Winter E.E.,

RA Webber C., Brandt P., Nyakatura G., Adetobi M., Chiaromonte F.,

RA Elnitski L., Eswara P., Hardison R.C., Hou M., Kolbe D., Makova K.,  
RA Miller W., Nekrutenko A., Riemer C., Schwartz S., Taylor J., Yang S.,  
RA Zhang Y., Lindpaintner K., Andrews T.D., Caccamo M., Clamp M.,  
RA Clarke L., Curwen V., Durbin R.M., Eyraas E., Searle S.M., Cooper G.M.,  
RA Batzoglu S., Brudno M., Sidow A., Stone E.A., Payseur B.A.,  
RA Bourque G., Lopez-Otin C., Puente X.S., Chakrabarti K., Chatterji S.,  
RA Dewey C., Pachter L., Bray N., Yap V.B., Caspi A., Tesler G.,  
RA Pevzner P.A., Haussler D., Roskin K.M., Baertsch R., Clawson H.,  
RA Furey T.S., Hinrichs A.S., Karolchik D., Kent W.J., Rosenbloom K.R.,  
RA Trumbower H., Weirauch M., Cooper D.N., Stenson P.D., Ma B., Brent M.,  
RA Arumugam M., Shteynberg D., Copley R.R., Taylor M.S., Riethman H.,  
RA Mudunuri U., Peterson J., Guyer M., Felsenfeld A., Old S., Mockrin S.,  
RA Collins F.S.;  
RT "Genome sequence of the Brown Norway rat yields insights into  
RT mammalian evolution.";  
RL Nature 428:493-521(2004).  
RN [2]  
RP IDENTIFICATION.  
RX PubMed=14981236; DOI=10.1073/pnas.0308746101;  
RA Bera T.K., Das S., Maeda H., Beers R., Wolfgang C.D., Kumar V.,  
RA Hahn Y., Lee B., Pastan I.;  
RT "NGEP, a gene encoding a membrane protein detected only in prostate  
RT cancer and normal prostate.";  
RL Proc. Natl. Acad. Sci. U.S.A. 101:3059-3064(2004).  
CC -!- FUNCTION: May play a role in cell-cell interactions (By  
CC similarity).  
CC -!- SUBCELLULAR LOCATION: Cell membrane; Multi-pass membrane protein  
CC (By similarity). Note=Concentrates at sites of cell-cell contact  
CC (By similarity).  
CC -!- SIMILARITY: Belongs to the TMEM16 family.  
CC -----  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC -----  
DR EMBL; AABR03068351; -; NOT\_ANNOTATED\_CDS; Genomic\_DNA.  
DR EMBL; AABR03069029; -; NOT\_ANNOTATED\_CDS; Genomic\_DNA.  
DR EMBL; AABR03070767; -; NOT\_ANNOTATED\_CDS; Genomic\_DNA.  
DR EMBL; BK004074; DAA04565.1; -; mRNA.  
DR UniGene; Rn.163084; -.  
DR Ensembl; ENSRNOG00000023427; Rattus norvegicus.  
DR RGD; 1302987; Ngep.  
DR InterPro; IPR007632; DUF590.  
DR PANTHER; PTHR12308; DUF590; 1.  
DR Pfam; PF04547; DUF590; 1.  
PE 2: Evidence at transcript level;  
KW Membrane; Transmembrane.  
FT CHAIN 1 860 Transmembrane protein 16G.  
FT /FTId=PRO\_0000289328.  
FT TOPO\_DOM 1 297 Extracellular (Potential).  
FT TRANSMEM 298 318 Potential.  
FT TOPO\_DOM 319 362 Cytoplasmic (Potential).  
FT TRANSMEM 363 383 Potential.  
FT TOPO\_DOM 384 441 Extracellular (Potential).  
FT TRANSMEM 442 462 Potential.  
FT TOPO\_DOM 463 492 Cytoplasmic (Potential).  
FT TRANSMEM 493 513 Potential.

FT	TOPO_DOM	514	530	Extracellular (Potential).
FT	TRANSMEM	531	551	Potential.
FT	TOPO_DOM	552	652	Cytoplasmic (Potential).
FT	TRANSMEM	653	673	Potential.
FT	TOPO_DOM	674	701	Extracellular (Potential).
FT	TRANSMEM	702	722	Potential.
FT	TOPO_DOM	723	779	Cytoplasmic (Potential).
FT	TRANSMEM	780	800	Potential.
FT	TOPO_DOM	801	860	Extracellular (Potential).
SQ	SEQUENCE	860 AA;	97170 MW;	96BE3CBD6DE96101 CRC64;
Query Match		76.0%;	Score 3764;	DB 1; Length 860;
Best Local Similarity		82.7%;	Pred. No. 4.3e-300;	
Matches	714;	Conservative	47;	Mismatches 94; Indels 8; Gaps 4;

Qy	55	MLRRRAQEEDSTVLIDVSPPEAEKRGSYGSTAHASEPGGQQAACRAGSPAKPRIADFVL	114
Db	1	MLRKQAGEEDSVVLIDMTSPEAGNGCSYGSTAQASEAGKQQVAPSRVGSSANPPI-DFVL	59
Qy	115	VWEEDLKLDRQQDSAARDRTDMHRTWRETFLDNLRAAGLCVDQQDVQDGNTTVHYALLSA	174
Db	60	VWEEDL---RSRENPTQDKTDTHEIWRETFLLENLRVAGLKIDQRDVQDEAAAVHYILLSA	116
Qy	175	SWAVLCYYAEDLRLKLPLQELPNQASNWSAGLLAWLGIPNVLLEVVPDPPEYYSCRFRV	234
Db	117	PWAVLCYYAEDLRLKLPLQELPNQASNWSATLLEWLGINLLENVDPDTPPEYYSCQFKA	176
Qy	235	NKLPRFLGSDNQDTFFTSTKRHQILFEILAKTPYGHEKKNLLGIHQLLAEGVLSAAFPLH	294
Db	177	SKLQWFLGSDNQDTFFTSTKRHQILFEILAKTPYGHQKKGLFGIDQLLAEGVFSAAFPLH	236
Qy	295	DGPFKTPPEGPQAPRLNQVLFQHWARWGKWNKYQPLDHVRRYFGEKVALYFAWLGFYT	354
Db	237	DGPFSVVPESQVLGLTQRQVLFKHWARWGKWRKYQPLDHVRRYFGEKVALYFAWLGFYT	296
Qy	355	GWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPLCLDCPFWLLSSACALAQA	414
Db	297	GWLLPAAVVGTVVFLAGCFLVFSDVPTQELCHSSDTFDMCPLCSDCSFWLLSSACTLAQA	356
Qy	415	GRLFDHGGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCSDYEDTEERPRPQFAASAPM	474
Db	357	GRLFDHGGTVFFSLFMALWAVLLLEYWKRKNATLAYRWDCSDYEDIEERPRPQFAATAPM	416
Qy	475	TAPNPITGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLVSIILYRAIMAIIVSRSGN	534
Db	417	TALNPITGEDEPYFPEKNRVRRLAGSVVLLMMVAVVIMCLVSIILYRAVMAIIVSKSNN	476
Qy	535	TLLAAWASRIASLTGSVVNLVFIILSKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIF	594
Db	477	AFLSAWASRIASLTGSVVNLVFIILSKVYVILAQVLTRWEMHRTQTAFEDAFTLKVFIF	536
Qy	595	QFVNFYSSPVYIAFFKGRFVGYPGNYHTLFGVRNEECAAGGCLIELAQELLVIMVGKQVI	654
Db	537	QFVNFYASPVYIAFFKGRFVGYPGNYHTLFGVRNEECAPAGGCLSELAQELLVIMVGKQII	596

## A6OLE6 BOVIN

```

ID      A6QLE6_BOVIN                               Unreviewed;          920 AA.
AC      A6QLE6;
DT      21-AUG-2007, integrated into UniProtKB/TrEMBL.
DT      21-AUG-2007, sequence version 1.
DT      21-AUG-2007, entry version 1.
DE      Putative uncharacterized protein.
OS      Bos taurus (Bovine).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC      Pecora; Bovidae; Bovinae; Bos.
OX      NCBI_TaxID=9913;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=L1 Hereford; TISSUE=Basal ganglia;
RA      Moore S., Alexander L., Brownstein M., Guan L., Lobo S., Meng Y.,
RA      Tanaguchi M., Wang Z., Yu J., Prange C., Schreiber K., Shenmen C.,
RA      Wagner L., Bala M., Barbazuk S., Barber S., Babakaiff R., Beland J.,
RA      Chun E., Del Rio L., Gibson S., Hanson R., Kirkpatrick R., Liu J.,
RA      Matsuo C., Mayo M., Santos R.R., Stott J., Tsai M., Wong D.,
RA      Siddiqui A., Holt R., Jones S.J., Marra M.A.;
RL      Submitted (JUN-2007) to the EMBL/GenBank/DDBJ databases.
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NoDerivs License
CC      -----
DR      EMBL; BC147937; AAI47938.1; -; mRNA.
PE      2: Evidence at transcript level;
SQ      SEQUENCE      920 AA;  107708 MW;  3AFFC6310F1862CD CRC64;

```

http://es/ScoreAccessWeb/GetItem.action?AppId=10552...4\_083148\_us-10-552-515-1.rup&ItemType=4&startByte=0 (12 of 41) 10/10/2008 8:48:54 AM

Qy	44	TSSGSHCARSRMLRRRAQEEDSTVLID----VSPPEAE-----KRGSYGST---AHASEP	91
Db	4	SSSGITNGRTRVFHPVA--KDVNILFDELEAVNSPCKDDDSLHPGNLTSTSDDASRLEA	61
Qy	92	GGQQAACRAGSPAKPRI-----ADFLVWEEEDLKLD RQQDSAARDRTDMHRTW	140
Db	62	GGETV-----PEKNKLNGLYFRDGKCRIDYILVYR---KSNPQMEK-----	99
Qy	141	RETFLDNLRAGLCVDQQDVQDGNTTVHYALLSASWAVLCYYAEDLRLKLPLQE---LP	196
Db	100	REVFERNIRAEGLOMEKESSLI-NSDIIFVKLHAPWEVLGRYAEQMNVRMPFRRKIYYLP	158
Qy	197	NQASNWS-----AGLLAWLGIPNVLL--EVVPDVPP-EYYSRFRVKNLPRFLGSDNQD	247
Db	159	RRYKFMSRIDKQISRFRRWLPKKPMRLDKETLPDLEENDCYTAPFSQQRRIHFI-IHNKD	217
Qy	248	TFFTSTKRHQILFEILAKTPYGHEKKNLLGIHQLLAEGVLSAAFPLHDGPFKTPPEGPQA	307
Db	218	TFFNNATRSRIVHHILQRIKY-EEGKNKIGLNRLLTNGSYEAAFPLHEGSYRSKNSIRTH	276
Qy	308	PRLNQQRQVLFQHWARWGKWNKYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPAAVVGTLV	367
Db	277	GAVNHRHLLYECWASWGVWYKYQPLDLVRRYFGEKIGLYFAWLGWYTGMLFPAAFGLFV	336
Qy	368	FLVGCFLVFSDIPTQELCGSKDSFEMCPLC-LDCPFWLLSSACALAQAGRLFDHGGTVFF	426
Db	337	FLYGVITLDHCQVSKEVCQATDII-MCPVCDKYCPFMRLSDSCVYAKVTHLFDNGATVFF	395
Qy	427	SLFMALWAVLLLEYWKRKSATLAYRWDCSDYEDTEERPRPQFAAS-APMTAPNPITGEDE	485
Db	396	AVFMAVWATVFLFWKRRRAVIAYDWDLIDWEEEEEEIRPQFEAKYSKKERMNPISGKPE	455
Qy	486	PYFPERSRARRMLAGSVVIVVMVAVVVMCLVSIILYRAIMAVVSRSGNTLLA-AWA---	541
Db	456	PYQAFADKCSRLIVSASGIFFMICVVIAAVFGIVIVRVTV-----STFAAFKWALIR	508
Qy	542	--SRIASLTGSVV--NLVFILILSKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFV	597
Db	509	NNSQVAT-TGTAVCINFCIIMLLNVLYEKVALLLTNLEQPRTESEWENSFTLKMFLFQFV	567
Qy	598	NFYSSPVYIAFFKGRFVGYPGNYHTLFG-VRNEECAAGGCLIELAQELLVIMVGKQVINN	656
Db	568	NLNSSTFYIAFFLGRFTGHPGAYLRLINRWRL ECHPSGCLIDL CMQMGIIIMVLKQTWNN	627
Qy	657	MQEVLPKPKLKGWWQKFLRLSKKRKAGASAGASQGPWEDDYELVPCE--GLFDEYLEMVLQ	714
Db	628	FMELGYPLIQNWWTR--RKVRQEHGPERKISFPQWEKDYNLQPMNAYGLFDEYLEMILQ	684
Qy	715	FGFVTIFVAACPLAPL FALNNWVEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTH	774
Db	685	FGFTTIFVAAFPLAPLLALLNNIIEIRLDAYKFVTQWRRPLASRAKDIGIWYGILEGIGI	744
Qy	775	LAVISNAFLLAFFSSDFLPRAYYRW-----TRAHDLRGFLNFTLA-----	813
Db	745	LSVITNAFVIAITSDFIPRLVYAYKYGPCAGQGEAGQKCMVGYVNASLSVFRISDFENRS	804

Qy 814 ---RAPSSFAAAHNRTCryRAFRDDDDGH-----YSQTYWNLLAIRLAFVIVFEHVVSFG 865  
| | : : | | | : | | : | : | | | | : | | :  
Db 805 EPESDGSEFSGTPLKYCRYRDYRDPHSLVPYGYTLQFWHVLAARLAFIIVFEHLVFCIK 864  
  
Qy 866 RLLDLLVPDIPESVEIKVKREYYLAKQALAENEVLFGTNGTKDEQPKGSELSSHW 920  
| : | : | | : : : : | | : : : | : : | : | :  
Db 865 HLISYLIPDLPKDLRDRMRREKYLIQEMMYEAELERLQKERKERKKNGKAHHNEW 919

RESULT 5

Q1AP36\_STRPU

ID Q1AP36\_STRPU Unreviewed; 903 AA.  
AC Q1AP36;  
DT 11-JUL-2006, integrated into UniProtKB/TrEMBL.  
DT 11-JUL-2006, sequence version 1.  
DT 24-JUL-2007, entry version 6.  
DE 122 kDa protein TMEM16 (Fragment).  
OS Strongylocentrotus purpuratus (Purple sea urchin).  
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
OC Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;  
OC Strongylocentrotus.  
OX NCBI\_TaxID=7668;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Coelomocyte;  
RA Galindo B.E., Moy G.W., Vacquier V.D.;  
RT "A 122 kDa protein from Strongylocentrotus purpuratus embryo belongs  
RT to TMEM16 protein family."  
RL Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.  
CC -----  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC -----  
DR EMBL; DQ020165; AAY82886.1; -; mRNA.  
DR UniGene; Spu.15325; -.  
DR InterPro; IPR007632; DUF590.  
DR PANTHER; PTHR12308; DUF590; 1.  
DR Pfam; PF04547; DUF590; 1.  
PE 2: Evidence at transcript level;  
FT NON\_TER 1 1  
SQ SEQUENCE 903 AA; 104887 MW; 443A4A4A7E50074A CRC64;

Query Match 30.8%; Score 1525.5; DB 2; Length 903;  
Best Local Similarity 38.1%; Pred. No. 9.3e-116;  
Matches 338; Conservative 161; Mismatches 304; Indels 85; Gaps 21;

Qy 61 QEEDSTVLIDVSPPEAEKRGSYGSTAHASEPGGQQAACRAGSPAK----- 106  
| : : | : | | : : | : | : | : | :  
Db 17 QPDNAAV---ANPQEIEM-----AESHMGAPTDKEDQPLHEGSPAKKDDNKVNDLFFKDG 68  
  
Qy 107 PRIADFVLVWEEDLKLDQQDSAARDRTDMHRTWRETFLDNLRAAGLCVD---QQDVQDG 163  
| | | | : | : | | : : | : | | | : : | :  
Db 69 KRRIDFVLAY-----RKQESEEREKRVKK--RQNFEANLIDEGQLQLEYENSEESHG 119  
  
Qy 164 NTTVHYALLSASWAVLCYYAEDLRLKLPLQELPNQASNWSAGLLAWLGIPNVLLEVVPDV 223

Db	120	RT--FFVKVHAPWDLMTTRYAEELKIKMPIEENNMEEPVNVFNCLDKLWTPFELSEEYVKP	177
Qy	224	PPEYYSCRFRVKNLPRFLGSDNQDTFFTSTKRHQILFEILAKTPYGHEKKNLLGIHQLLA	283
Db	178	EPDVFTAPFIRDRASEFI-MESQDTFFPNNIRNRVVEILERMRYDANDPAKFGIDHLIA	236
Qy	284	EGVLSAAFPPLHDGPFKTP----PEGPQAPRLNQVLFQHWARWGKWNKYQPLDHVRRYF	339
Db	237	NGSYFAAYPLHEGDYKSKHSLTHGPQ----NDRHLLYEEWARPGRWYKKQPLDLIRRYF	292
Qy	340	GEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPLC-L	398
Db	293	GEKIGIYFCWLGFYTEMLTWAGFVGLIVFLYGCISLPSSVVVQEICDGTDI-MCPLCDK	351
Qy	399	DCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCSDYE	458
Db	352	RCPYWTLSDSCFYSKLTYLFDNEATVFFACFMSLWATMFCFWKRRQNTIDYDWDLFGFE	411
Qy	459	DTEERPRPQFAASAPMTAPNPITGEDEPYFPERSRARRMLAGSVVIVVMVAVVMCLVSI	518
Db	412	EQEENIRPEFEAKAPDRRVSPITNLTEPYMKFSRKFPFRFSASIASIFFMILLVMAAVMTV	471
Qy	519	ILYRAIMAIIVSRSGNTLLAAWASRIASLTGSVVNLVFILILSKIYVSLAHVLTRWEMHR	578
Db	472	IVYRIVVKTAIFAIDQEFISSYASIITSVTASMISLILIMILQILYERIAVWLTNLELHR	531
Qy	579	TQTKFEDAFTLKVFIFQFVNFYSSPVYIAFFKGRFVGYPGNYHTLFGV-RNEECAAGGCL	637
Db	532	TETEDSFTFKMYLFAFVNYYSTSFYIAFFKGRLPGTPADYGRVFGIWRQEECDPAGCM	591
Qy	638	IELAQELLVIMVGKQVINNMQEVLIPLKLGWWQKFRRLRSKKRKAGASAGASQGPWEDDYE	697
Db	592	QELFINIAITMCGKQFFNNFMELAMPVLMNFWRS-RTGRKEEKSGK---GRYEQWEQDAD	647
Qy	698	LVPC--EGLFDEYLEMVLQFGFVTIFVAACPLAPL FALLNNWVEIRLDARKFVCEYRRPV	755
Db	648	LADLGPRGLFKEYLEMVVQFGFSTIFVAAPLAPL FALLNNLVEVRLDAYKFISQLRRPV	707
Qy	756	AERAQDIGIWFHILAGLTHLAVISNAFLAFSSDFLPR--AYRWTRAHDLRGFLNFTL	812
Db	708	AKRAQDIGAWYAILVTGNLSVLTNALVIAFTSEFIPRQVFKYYYGGPEATLNGYTNWSL	767
Qy	813	A-----RAPSSFAAAHNRT-----CRYRAFRDDDDGHYSQT--YWNL	846
Db	768	SYFNTVDMQNDSKPTDPSYPRVGDEDTTDPNYGLNVSVCRYRGNYDE--HYNVTLDYWL	825
Qy	847	LAIRLAFVIVFEHVVFVSVGRLLDLLVPDIPESVEIKVKREYYLAKQAL	894
Db	826	IAIKLAFILLYEHFVLF TKFFVAYIIPDMPEFVKNQIKRETYLGQQAL	873

RESULT 6

TM16D\_HUMAN

ID TM16D\_HUMAN

Reviewed;

955 AA.

AC Q32M45; Q8NAJ0; Q8NB39; Q8NB53;  
 DT 29-MAY-2007, integrated into UniProtKB/Swiss-Prot.  
 DT 06-DEC-2005, sequence version 1.  
 DT 21-AUG-2007, entry version 17.  
 DE Transmembrane protein 16D.  
 GN Name=TMEM16D;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
 OC Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS 2 AND 3).  
 RC TISSUE=Brain, and Prostate;  
 RX PubMed=14702039; DOI=10.1038/ng1285;  
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,  
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,  
 RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,  
 RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,  
 RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,  
 RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,  
 RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,  
 RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,  
 RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,  
 RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,  
 RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,  
 RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y.,  
 RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,  
 RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,  
 RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,  
 RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,  
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,  
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,  
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,  
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,  
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,  
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,  
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,  
 RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,  
 RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,  
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,  
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,  
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;  
 RT "Complete sequencing and characterization of 21,243 full-length human  
 RT cDNAs.";  
 RL Nat. Genet. 36:40-45(2004).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).  
 RX PubMed=15489334; DOI=10.1101/gr.2596504;  
 RG The MGC Project Team;  
 RT "The status, quality, and expansion of the NIH full-length cDNA  
 RT project: the Mammalian Gene Collection (MGC).";  
 RL Genome Res. 14:2121-2127(2004).  
 RN [3]  
 RP IDENTIFICATION.  
 RX PubMed=12739008;



```

RA   Katoh M., Katoh M.;
RT   "FLJ10261 gene, located within the CCND1-EMS1 locus on human
RT   chromosome 11q13, encodes the eight-transmembrane protein homologous
RT   to C12orf3, C11orf25 and FLJ34272 gene products.";
RL   Int. J. Oncol. 22:1375-1381(2003).
CC   -!- SUBCELLULAR LOCATION: Membrane; Multi-pass membrane protein
CC       (Potential).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=3;
CC       Name=1;
CC       IsoId=Q32M45-1; Sequence=Displayed;
CC       Name=2;
CC       IsoId=Q32M45-2; Sequence=VSP_025742;
CC       Name=3;
CC       IsoId=Q32M45-3; Sequence=VSP_025741, VSP_025743;
CC       Note=No experimental confirmation available;
CC   -!- SIMILARITY: Belongs to the TMEM16 family.
CC   -----
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   -----
DR   EMBL; AK091540; BAC03688.1; ALT_INIT; mRNA.
DR   EMBL; AK091591; BAC03704.1; -; mRNA.
DR   EMBL; AK092596; BAC03924.1; -; mRNA.
DR   EMBL; BC109308; AAI09309.1; -; mRNA.
DR   UniGene; Hs.58785; -.
DR   Ensembl; ENSG00000151572; Homo sapiens.
DR   HGNC; HGNC:23837; TMEM16D.
DR   MIM; 610111; gene.
DR   PharmGKB; PA134975112; -.
DR   ArrayExpress; Q32M45; -.
DR   InterPro; IPR007632; DUF590.
DR   PANTHER; PTHR12308; DUF590; 1.
DR   Pfam; PF04547; DUF590; 1.
PE   2: Evidence at transcript level;
KW   Alternative splicing; Coiled coil; Glycoprotein; Membrane;
KW   Polymorphism; Transmembrane.
FT   CHAIN           1           955       Transmembrane protein 16D.
FT                                     /FTId=PRO_0000288650.
FT   TRANSMEM        353        373       Potential.
FT   TRANSMEM        425        445       Potential.
FT   TRANSMEM        506        526       Potential.
FT   TRANSMEM        548        568       Potential.
FT   TRANSMEM        596        616       Potential.
FT   TRANSMEM        716        736       Potential.
FT   TRANSMEM        769        789       Potential.
FT   TRANSMEM        886        906       Potential.
FT   COILED          918        953       Potential.
FT   CARBOHYD        824        824       N-linked (GlcNAc . . .) (Potential).
FT   VAR_SEQ          1         433       Missing (in isoform 3).
FT                                     /FTId=VSP_025741.
FT   VAR_SEQ         19         54       EGGVDLQGYQLDMQILPDGPKSDVDFSEILNAIQEM -> V
FT                                     (in isoform 2).
FT                                     /FTId=VSP_025742.
FT   VAR_SEQ        466        512       Missing (in isoform 3).

```

FT /FTId=VSP\_025743.  
FT VARIANT 115 115 G -> A (in dbSNP:rs34162417).  
FT /FTId=VAR\_032453.  
FT CONFLICT 209 209 F -> L (in Ref. 1; BAC03704).  
SQ SEQUENCE 955 AA; 111462 MW; 9A9348C61A4F20AF CRC64;

Query Match 30.8%; Score 1525.5; DB 1; Length 955;  
Best Local Similarity 38.2%; Pred. No. 1e-115;  
Matches 355; Conservative 163; Mismatches 309; Indels 103; Gaps 28;

Qy 63 EDSTVLID----VSPPEAE-----KRGSYGST---AHASEPGGQQAACRAGS-----PA 105  
:| :| | ||| : | :| | | | : :  
Db 56 KDVNILFDELEAVSSPCKDDDSLHPGNLTSTSDDASRL EAGGETVPERNKSNGLYFRDG 115

Qy 106 KPRIADFVLVWEEDLKLDRQQDSAARDRTDMHRTWRETFLDNLRAAGLCVDQQDVQDGNT 165  
| ||| :||: : : :| : || | | :|| || :|| :| :  
Db 116 KCRI-DYILVYRK-----SNPQTEK----REVFERNIRA EGLQMEKESSLI-NS 158

Qy 166 TVHYALLSASWAVLCYYAEDLRLKLPLQE----LPNQASNWS-----AGLLAWLGIPNV 215  
: : | | | || ||| : :|| : || : | : || :  
Db 159 DIIFVKLHAPWEVLGRYAEQMNVRMPFRRKIYYLPRRYKFMSRIDKQISRFRRWLPKKPM 218

Qy 216 LL--EVVPDVPP-EYYSCRFRVNKLPRFLGSDNQDTFFTSTKRHQILFEILAKTPYGHEK 272  
| | :||: : | : :| : | :||| : | :| : || : | |  
Db 219 RLDKETLPDLEENDCYTAPFSQQRIHHFI-IHNKETFFNNATRSRIVHHILQRIKY-EEG 276

Qy 273 KNLLGIHQLLAEGVLSAAFP LHDGPFKTPPEGPQAPRLNQRQVLFQHWARWGKWNKYQPL 332  
|| :||::|| | ||||| :| :|| : || :||| || ||| |||||  
Db 277 KNKIGLNRLLTNGSYEAAFP LHEGSYRSKNSIRTHGAENHRHLLYECWASWGVYKYQPL 336

Qy 333 DHVRRYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSKDSFE 392  
| ||||| :| :||| :||| | ||| :| ||| | : :||:| :|  
Db 337 DLVRRYFGEKIGLYFAWLGWYTGM LFPAAFIGLFVFLYGVTTLDHSQVSKEVCQATDII- 395

Qy 393 MCPLC-LDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSATLAYR 451  
||| :| ||| || :| | : ||| :| |||| :||| :| :||| :| :||  
Db 396 MCPVCDKYCPFMRLSDSCVYAKVTHLFDNGATVFFAVFMAVWATVFLEFWKRRRAVIAYD 455

Qy 452 WDCSDYEDTEERPRPQFAAS-APMTAPNPITGEDEPYFPERSRARRMLAGSVVIVVMVAV 510  
|| | :| : || |||| | : ||| :| ||| : | :| : | :| :|  
Db 456 WDLIDWEEEEEEIRPQFEAKYSKKERMNPISGKPEPYQAFTDKCSRLIVSASGIFFMICV 515

Qy 511 VVMCLVSIILYRAIMAIVVSRSNGNTLLA-AWA-----SRIASLTGSVV--NLVFILILSK 562  
| : : | :|| : :| | || | :|| :||| | | | :|| :  
Db 516 VIAAVFGIVIIYRVVTV-----STFAAFKWALIRNNSQVAT-TGTAVCINFCIIMLLNV 567

Qy 563 IYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIQFVNFIYSSPVYIAFFKGRFVGYPGNYHT 622  
:| :| :|| | ||::|| :||| :| |||| || |||| ||| | :||| |  
Db 568 LYEKVALLLTNLEQPRTESEWENSFTLKMFLFQFVNLSSTFYIAFFLGRFTGHPGAYLR 627

Qy 623 LFG-VRNEECAAGGCLIELAQELLVIMVGKQVINNMQEVLPKLGWWQKFRLRSKKRKA 681  
| | ||| |||| :| : :||| || || | : | :| :| :| :|| :||  
Db 628 LINRWRLEECHPSGCLIDLQMGIIMVLKQTWNNFMELGYPLIQNWWTR---RKVRQEH 684

Qy 682 GASAGASQGPWEDDYELVPCE--GLFDEYLEMVLQFGFVTIFVAACPLAPL FALLNNWVE 739  
| | | ||| | | ||||| :||| ||||| ||||| ||||| ||||| :|

```

ID      Q1AP35_STRPU                               Unreviewed;              921 AA.
AC      Q1AP35;
DT      11-JUL-2006, integrated into UniProtKB/TrEMBL.
DT      11-JUL-2006, sequence version 1.
DT      24-JUL-2007, entry version 6.
DE      122 kDa protein TMEM16.
OS      Strongylocentrotus purpuratus (Purple sea urchin).
OC      Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC      Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
OC      Strongylocentrotus.
OX      NCBI_TaxID=7668;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RC      TISSUE=Testis;
RA      Galindo B.E., Vacquier V.D.;
RT      "Phylogeny of the TMEM16 Protein Family: Some Are Over Expressed in
RT      Cancer.";
RL      Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NoDerivs License
CC      -----
DR      EMBL; DQ020166; AAY82887.1; -; mRNA.
DR      UniGene; Spu.15325; -.
DR      InterPro; IPR007632; DUF590.
DR      PANTHER; PTHR12308; DUF590; 1.
DR      Pfam; PF04547; DUF590; 1.
PE      2: Evidence at transcript level;
SQ      SEQUENCE      921 AA;  106711 MW;  C3F912A32528F059 CRC64;

```

http://es/ScoreAccessWeb/GetItem.action?AppId=10552...4\_083148\_us-10-552-515-1.rup&ItemType=4&startByte=0 (19 of 41)10/10/2008 8:48:54 AM

Qy	61	QEEDSTVLIDVSPPEAEKRGSYGSTAHASEPGGQQAACRAGSPAK-----	106
		:::   :     : :   : :	
Db	26	QPDNAAV---ANPQEIEM-----AESHMGAPTDKEDQPLHEGSPAKKDDNKVNDLFFKDG	77
Qy	107	PRIADFLVWEEEDLKLD RQQDSAARDRTDMHRTWRETFLDNLRAAGLCV-----	155
		:   :     : :   :       :	
Db	78	KRRIDFVLAY-----RKQESEEREKRVKK--RQNFEANLIDEGQLQLEYENSEGPEPK	128
Qy	156	-DQQDVQDGNTTVHYALLSASWAVLCYYAEDLRLKLPLQELPNQASNWSAGLLAWLGIPN	214
		:       : :     : :     : :   : :   : :   :	
Db	129	EDDPESH DGR T--FFVKVHAPWDL MTRYAEELKIKMPIEENNMEEPVN VFNCIDKLWTPF	186
Qy	215	VLLEVVPDVPPEYYSCRFRV NKLPRLFGSDNQDTFFTSTKRHQILFEILAKTPYGHEKKN	274
		: :   : :   : :         :   : :     :	
Db	187	ELSEEYVKPEPDVFTAPFIRDRASEFI-MESQDTFFPNNIRNRVVEILERMRYDANDPA	245
Qy	275	LLGIHQLLAEGVLSAAFP LHDGPFKTP----PEGPQAPRLNQ RQVLFQHWARWGKWNKYQ	330
		:       :     : :           : :	
Db	246	KFGIDHLIANGSYFAAYPLHEGDYKSKHSL LTHGPQ----NDRHLLYE EWARPGRWYKKQ	301
Qy	331	PLDHVRRYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSKDS	390
		:         : :                 :     :   :	
Db	302	PLDLIRRYFGEKIGIYFCWLGFYTEMLTWAGFVGLIVFLYGCISLPSSVVVQEICAGTDI	361
Qy	391	FEMCPLC-LDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSATLA	449
		:     :   : :     :     :     :   :	
Db	362	I-MCPLCDKRCPYWTLSDSCFYSKLTYLFDNEATVFFACFMSLWATMFCEFWKRRQNTID	420
Qy	450	YRWDCSDYEDTEERPRPQFAASAPMTAPNPITGEDEPYFPERSRARRMLAGSVVIVVMVA	509
		: :       :       :       :       :	
Db	421	YDWDLFGFEEQEENIRPEFEAKAPDRRVSPITNLTEPYMKFSRKFP RFSASIASIFFMIL	480
Qy	510	VVVMCLVSIILYRAIMAI VVSRSNTLLAAWASRIASLTGSV VNLVFILILSKIYVSLAH	569
		:   : : : :   :   : : :       :     : :   :   :	
Db	481	LVMAAVMTVIVYRIVVKTAIFAIDQEFISSYASIITSVTASMISLILIMILQILYERIAV	540
Qy	570	VLTRWEMHRTQTKFEDAFTLKVFIFQFVN FYSSPVYIAFFKGRFVGYPGNYHTLFGV-RN	628
		:     :   :     : :     :                 :   :	
Db	541	RLTNLELHRTET EYEDSFTFKMYLFAFVNYYSTSFYIAFFKGRLP GTPADYGRVFGIWRQ	600
Qy	629	EECAAGGCLIELAQELLVIMVGKQVINNMQEV LIPKLKGWWQKFR LRSKKRKAGASAGAS	688
		:     : :           : :     :   :	
Db	601	EECDPAGCMQELFINIAITMCGKQFFNFMELAMPVLMNFWRS-RTGRKEEKSGK--GR	656
Qy	689	QGPWEDDYELVPC--EGLFDEYLEMV LQFGFVTIFVAACPLAPL FALLNNWVEIRLDARK	746
		:             :	
Db	657	YEQWEQDADLADLGRPLGFKEYLEMVVQFGFSTIFVA AFPLAPL FALLNNLVEVRLDAYK	716
Qy	747	FVCEYRRPVAERAQDIGIWFHILAGLTHLAVISNAFL LAFSSDFLPR---AYRWTRAHD	803
		: :         :         :     : :   :   :   :	
Db	717	FISQLRRPVAKRAQDIGAWYAILVTVGNLSVLTNALVIAFTSEFIPRQVF KYYYGGPEAT	776
Qy	804	LRGFLNFTLA-----RAPSSFAAAHNRT-----CRYRAFRDDDGHY	839
		:   :   :                           :	
Db	777	LNGYTNWSLSYFNTVDMQNDSKPTDPSYPRVGDEDTTDPNYGLNVSVCRYRGNYDE--HY	834

Qy 840 SQT--YWNLLAIRLAFVIVFEHVVFVSVGRLLDLLVPDIPESVEIKVKREYYLAKQAL 894  
: | || ::||:||||:|||| | : ::||:|| |: ::||| || :|||  
Db 835 NVTLDYWLVIAlKLAfILLYEHfVLfTKFFVAYIIPDMPEfVKNQIKRETYLGQQAL 891

RESULT 8

A2AHE5\_MOUSE

ID A2AHE5\_MOUSE Unreviewed; 981 AA.  
AC A2AHE5;  
DT 20-FEB-2007, integrated into UniProtKB/TrEMBL.  
DT 20-FEB-2007, sequence version 1.  
DT 21-AUG-2007, entry version 6.  
DE Novel protein (B230324K02Rik).  
GN Name=RP23-300M9.6; ORFNames=RP23-300M9.6-002;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muroidea; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Smith M.;  
RL Submitted (JUL-2007) to the EMBL/GenBank/DDBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RA Kay M.;  
RL Submitted (JUL-2007) to the EMBL/GenBank/DDBJ databases.  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RA Phillimore B.;  
RL Submitted (JUL-2007) to the EMBL/GenBank/DDBJ databases.  
CC -----  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC -----  
DR EMBL; AL731700; CAM18325.1; -; Genomic\_DNA.  
DR EMBL; AL731779; CAM18325.1; JOINED; Genomic\_DNA.  
DR EMBL; BX005257; CAM18325.1; JOINED; Genomic\_DNA.  
DR EMBL; AL731779; CAM25697.1; -; Genomic\_DNA.  
DR EMBL; AL731700; CAM25697.1; JOINED; Genomic\_DNA.  
DR EMBL; BX005257; CAM25697.1; JOINED; Genomic\_DNA.  
DR EMBL; BX005257; CAM27817.1; -; Genomic\_DNA.  
DR EMBL; AL731700; CAM27817.1; JOINED; Genomic\_DNA.  
DR EMBL; AL731779; CAM27817.1; JOINED; Genomic\_DNA.  
DR InterPro; IPR007632; DUF590.  
DR PANTHER; PTHR12308; DUF590; 1.  
DR Pfam; PF04547; DUF590; 1.  
PE 4: Predicted;  
SQ SEQUENCE 981 AA; 114568 MW; E851D80BC49F4977 CRC64;

Query Match 30.6%; Score 1512.5; DB 2; Length 981;  
Best Local Similarity 38.9%; Pred. No. 1.2e-114;  
Matches 333; Conservative 166; Mismatches 279; Indels 79; Gaps 25;

Qy 106 KPRIADFVLVWEEDLKLDRQQDSAARDRTDMHRTWRETFLDNLRAAGLCVDQQDVQDGNT 165

Db	161	KKRI-DYILVYR-----KTNIQYDKRNTFEKNLRAEGLMLEKEPA-IANP	203
Qy	166	TVHYALLSASWAVLCYYAEDLRLKLPLQ-----ELPNQASNWSAGLLAWLGIPNV	215
Db	204	DIMFIKIHIPWDTLCKYAERLNIRVPFRKKCYTQDKNKSRSRVQNYFKRIKKWMSQNPM	263
Qy	216	LLE--VVPDV-PPEYYSCRFRVNKLPRFLGSDNQDTFFTSTKRHQILFEILAKTPY--GH	270
Db	264	VLDKSAFPELEESDCYTGPFSRARIHHFI-INNKDTFFSNATRSRIVYHMLERTKYENGI	322
Qy	271	EKKNLLGIHQLLAEGVLSAAFPPLHDGPFKT----PPEGPQAPRLNQVLFQHWARWGKW	326
Db	323	SK---VGIRKLITNGSYIAAFPHEGAYKSSLPIKTHGPQ----NNRHLLYERWARWGMW	375
Qy	327	NKYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCG	386
Db	376	YKHQPLDLIRMYFGEKIGLYFAWLGWYTGM LIPAAVVGLCVFFYGLVTMNESQVSQEICK	435
Qy	387	SKDSFEMCPLC-LDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKS	445
Db	436	ATEVF-MCPLCDKNCSLQRLNDSCIYAKVTYLF DNGGTVFFAIFMAIWATVFLEFWKRRR	494
Qy	446	ATLAYRWDCCSDYEDTEERPRPQFAAS-APMTAPNPITGEDEPYFPERSRARRMLAGSVVI	504
Db	495	SILTYTWDLIEWEEEEETLRPQFEAKYYRMEVINPITGKPEPHQPSSDKVTRLLVSVSGI	554
Qy	505	VVMVAVVVMCLVSIILYR-AIMAIVVSRSNTLLAAWASRIASLTGSV-VNLVFILILSK	562
Db	555	FFMISLVITAVFAVVYRLVMEQFASFKNFVKQHW--QFATSGAAVCINFIIIMLLNL	612
Qy	563	IYVSLAHVLTWRWEMHRTQTKFEDAFTLKVFIFQFVNIFYSSPVYIAFFKGRFVGYPGNYHT	622
Db	613	AYEKIAYLLTNLEYPRTESEWENSFALKMFLFQFVNLNSSIFYIAFFLGRFVGHPGKYNK	672
Qy	623	LF-GVRNEECAAGGCLIELAQELLVIMVGKQVINNMQEVLPKLGWWQKFRRLRSKKRKA	681
Db	673	LFERWRLEECHPSGCLIDLCLQMGVIMFLKQIWNFMELGYPLIQNWWSRHKI-----KR	727
Qy	682	GASAGASQGPWEDDYELVP--CEGLFDEYLEMVLQFGFVTIFVAACPLAPL FALLNNWVE	739
Db	728	GIQ-DASIPQWENDWNLQPMNIHGLMDEYLEMVLQFGFTTIFVAAFPLAPLLALLNNIE	786
Qy	740	IRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISNAFLAFSSDFLPRAYYRW-	798
Db	787	IRLDAYKFVTQWRRPLPARATDIGIWL GILEGIGILAVITNAFVIAITS DYIPRFVY EYK	846
Qy	799	-----TRAHDLRGFLNFTLARAP-SSFAAAHNRTC RYRAFR-----DDDGHYSQTY	843
Db	847	YGPCANHV KQENENCLKG YVNNSLSFFDLSELGMGKSGYCRYR DYRGPPWSSKPYEFTLQY	906
Qy	844	WNLLAIRLAFVIVFEHVVS VGRLLDLLVPDIPESVEIKVKREYYLAKQALAENEVLFGT	903
Db	907	WHILAAARLAFIIVFEHLVFGIKSFIAYLIPDIPKGLRERIRREKYL VQEMMYEAE L--E	963
Qy	904	NGTKDEQPKGSELSSHW	920

Db                   :   :   :   |   :   |  
964 HLQQQRRKSGQPIHHEW 980

RESULT 9

TM16C\_HUMAN

ID    TM16C\_HUMAN                   Reviewed;                   981 AA.  
AC    Q9BYT9;  
DT    16-JAN-2004, integrated into UniProtKB/Swiss-Prot.  
DT    01-JUN-2001, sequence version 1.  
DT    24-JUL-2007, entry version 31.  
DE    Transmembrane protein 16C.  
GN    Name=TMEM16C; Synonyms=C11orf25; ORFNames=GENX-3947;  
OS    Homo sapiens (Human).  
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC    Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
OC    Catarrhini; Hominidae; Homo.  
OX    NCBI\_TaxID=9606;  
RN    [1]  
RP    NUCLEOTIDE SEQUENCE [MRNA].  
RA    Rosier M.F., Toselli E., Segurens-Soury B., Auffray C., Devignes M.D.;  
RT    "Predominant brain expression and full-length characterization of a  
RT    novel human 6.6-Kb transcript mapping at 11p14 in the telomeric part  
RT    of WAGR locus.";  
RL    Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.  
CC    -!- SUBCELLULAR LOCATION: Membrane; Multi-pass membrane protein  
CC    (Probable).  
CC    -!- SIMILARITY: Belongs to the TMEM16 family.  
CC    -----  
CC    Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC    Distributed under the Creative Commons Attribution-NoDerivs License  
CC    -----  
DR    EMBL; AJ300461; CAC32454.1; -; mRNA.  
DR    UniGene; Hs.91791; -.  
DR    Ensembl; ENSG00000134343; Homo sapiens.  
DR    KEGG; hsa:63982; -.  
DR    HGNC; HGNC:14004; TMEM16C.  
DR    MIM; 610110; gene.  
DR    PharmGKB; PA25489; -.  
DR    ArrayExpress; Q9BYT9; -.  
DR    InterPro; IPR007632; DUF590.  
DR    PANTHER; PTHR12308; DUF590; 1.  
DR    Pfam; PF04547; DUF590; 1.  
PE    2: Evidence at transcript level;  
KW    Membrane; Transmembrane.  
FT    CHAIN                   1       981           Transmembrane protein 16C.  
FT   /FTId=PRO\_0000072565.  
FT    TRANSMEM           398       420           Potential.  
FT    TRANSMEM           471       490           Potential.  
FT    TRANSMEM           553       575           Potential.  
FT    TRANSMEM           590       612           Potential.  
FT    TRANSMEM           642       664           Potential.  
FT    TRANSMEM           759       781           Potential.  
FT    TRANSMEM           809       831           Potential.  
FT    TRANSMEM           904       926           Potential.

SQ SEQUENCE 981 AA; 114655 MW; 15A3276420912393 CRC64;

Query Match 30.4%; Score 1504; DB 1; Length 981;  
 Best Local Similarity 39.4%; Pred. No. 6.1e-114;  
 Matches 329; Conservative 163; Mismatches 268; Indels 76; Gaps 24;

Qy 106 KPRIADFVLVWEEDLKLDRQQDSAARDRTDMHRTWRETFLDNLRAAGLCVDQQDVQDGNT 165  
 | ||| |::||: :|:: | || |||| || :::: :  
 Db 161 KRRI-DYILVYR-----KTNIPYDKRNTFEKNLRAEGLMLEKEPA-IASP 203

Qy 166 TVHYALLSASWAVLCYYAEDLRLKLPLQ-----ELPNQASNWSAGLLAWLGIPNV 215  
 : : : | || ||| |::| : : : : : | : :  
 Db 204 DIMFIKIHIPWDTLKYAERLNIRMPFRKKCYTGRSKSMGRMQTYFRRIKDWMAQNPM 263

Qy 216 LLE--VVPDV-PPEYYSCRFRVKNLPRFLGSDNQDTFFTSTKRHQILFEILAKTPY--GH 270  
 :|: ||: :|: | :: |: :|:||||: | :|: :| :| | |  
 Db 264 VLDKSAFPDLEESDCYTGFPSRARIHHFI-INNKDTFFSNATRSRIVYHMLERTKYENGI 322

Qy 271 EKKNLLGIHQLLAEGVLSAAFPLHDGPFKT----PPEGPQAPRLNQRVLFQHWARWGKW 326  
 | :|| |: | ||| |:| |: ||| | | :|: |||| |  
 Db 323 SK--VGIRKLINNGSYIAAFPPEGAYKSSQPIKTHGPQ----NNRHLLYERWARWGMW 375

Qy 327 NKYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCG 386  
 |:|||| :| ||||: |||||:|||| |:||:| | | : : :|:|  
 Db 376 YKHQPLDLIRLYFGEKIGLYFAWLGWYTGMLIPAAIVGLCVFFYGLFTMNNSQVSQEICK 435

Qy 387 SKDSFEMCPLC-LDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKS 445  
 : : | |||| :| |:| |: ||:|||||:|:|:| : |:|:|:  
 Db 436 ATEVF-MCPLCDKNCSLQRLNDSCIYAKVTYLFNNGGTVFFAIFMAIWATVFLEFWKRRR 494

Qy 446 ATLAYRWDCSDYEDTEERPRPQFAAS-APMTAPNPITGEDEPYFPERSRARRMLAGSVVI 504  
 : | | || ::|: || ||| | | ||||: ||: | : |:| |  
 Db 495 SILTYTWDLIEWEEEEETLRPQFEAKYYKMEIVNPITGKPEPHQPSSDKVTRLLVSVSGI 554

Qy 505 VVMVAVVVMCLVSIILYR-AIMAIVVSRSNTLLAAWASRIASLTGSV-VNLVFILILSK 562  
 |::|: : ::|| :| | : | :|: :| :| :|:|:  
 Db 555 FFMISLVITAVFGVVYRLVMEQFASFKNWFIKQYW--QFATSAAAVCINFIIIMLLNL 612

Qy 563 IYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNIFYSSPVYIAFFKGRFVGYPGNYHT 622  
 | :|:| | | ||::|:| ||:|:|||| | | |||| ||||:| | :  
 Db 613 AYEKIAYLLTNLEYPRTESEWENSFALKMFLFQFVNLNSSIFYIAFFLGRFVGHPGKYNK 672

Qy 623 LFG-VRNEECAAGGLIELAQELLVIMVGKQVINNMQEVLPKLGWWQKFRRLRSKKRKA 681  
 || | ||| |||:| :: || ||: || |: | :| || : : |  
 Db 673 LFDRWRLEECHPSGCLIDLCLQMGVIMFLKQIWNNFMELGYPLIQNWWSRHKI-----KR 727

Qy 682 GASAGASQGPWEDDYELVP--CEGLFDEYLEMVLQFGFVTIFVAACPLAPL FALLNNWVE 739  
 | || ||:|: | | || ||||| ||||| ||||| ||||| :|  
 Db 728 GIH-DASIPQWENDWNLQPMNLHGLMDEYLEMVLQFGFTTIFVAAFPLAPLLALLNNIIE 786

Qy 740 IRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISNAFLAFSSDFLPRAYYRW- 798  
 ||||| ||| :|:|: || |||| | | : |||:|:|:| :|:|:| | :  
 Db 787 IRLDAYKFVTQWRRPLPARATDIGIWLGILEGIGILAVITNAFVIAITSDYIPRFVYEYK 846

Qy 799 -----TRAHDLRGFLNFTLARAP-SSFAAAHNRTCryRAFR-----DDDGHYSTY 843  
 : |:|:|:| :|: | : ||| :| : : |



Db 847 YGPCANHVEPSENCLKGYVNNLSFFDLSELGMGKSGYCRYRDYRGPPWSSKPYEFTLQY 906

Qy 844 WNLLAIRLAFVIVFEHVVSFVGRLLDLLVPDIPESVEIKVKREYYLAKQALAEDEV 899  
|::|| |::|::||::|::| : : |::|::| : ::|| || :: : | |:

Db 907 WHILAAARLAFIIVFEHLVFGIKSFIAFLIPDVPKGLHDIRREKYLQEMMYEAEEL 962

RESULT 10

A1A5Z4\_DANRE

ID A1A5Z4\_DANRE Unreviewed; 900 AA.

AC A1A5Z4;

DT 23-JAN-2007, integrated into UniProtKB/TrEMBL.

DT 23-JAN-2007, sequence version 1.

DT 24-JUL-2007, entry version 6.

DE Zgc:158430.

GN ORFNames=zgc:158430;

OS Danio rerio (Zebrafish) (Brachydanio rerio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; Danio.

OX NCBI\_TaxID=7955;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Kidney;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Kidney;

RG NIH MGC Project;

RL Submitted (DEC-2006) to the EMBL/GenBank/DDBJ databases.

CC -----

CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>

CC Distributed under the Creative Commons Attribution-NoDerivs License

CC -----

DR EMBL; BC128870; AAI28871.1; -; mRNA.

DR UniGene; Dr.108272; -.  
DR ZFIN; ZDB-GENE-061215-108; zgc:158430.  
DR InterPro; IPR007632; DUF590.  
DR PANTHER; PTHR12308; DUF590; 1.  
DR Pfam; PF04547; DUF590; 1.  
PE 2: Evidence at transcript level;  
SQ SEQUENCE 900 AA; 105263 MW; DB86567CCE3D153E CRC64;

Query Match 30.3%; Score 1500.5; DB 2; Length 900;  
Best Local Similarity 38.0%; Pred. No. 1.1e-113;  
Matches 323; Conservative 170; Mismatches 266; Indels 91; Gaps 20;

Qy	108	RIADFVLVWEEDLKLD	RQQDSAARDRTDMHRTWRETFLDNLRAAGLCVDQQDVQDG-NTT	166
		: :  :  :: :	: :  : :	
Db	49	RRIDFVLSYVDDKEGD	KKAER-----RREFEANLEKAGLELETEDKSESDDRK	96
Qy	167	VHYALLSASWAVLCY	YAEDLRLKLPL-----QELPNQASNWSAGLLAWLGIPNVLLE	218
		:          :  ::  :	:  :	
Db	97	THYALKIHAPWEVLAT	YADVLIKIKVPFKVSDIPKAREVP-----LEWLSHPFRLPE	146
Qy	219	VVPDVPPEYYSCRFR	VNKLPRFLGSDNQDTFFTSTKRHQILFEILAKTPYGHE---KKNL	275
		:  ::   :  :     ::    :	::  :    :     :  :	
Db	147	NIMRPEPDYFTAPFD	KSKVDFFL-IDDKDTFFPPSTRNRIVYYILTRCPYYKEDRKEKDK	205
Qy	276	LGIHQLLAEGVLSAA	FPLHDGPFKTPPEGPQAPRLNQVLFQHWARWGKWNKYQPLDHV	335
		::    : ::    :	: :   :   ::    :       :	
Db	206	TGINRLNNGTYTSAY	PLHDCRYWKKAQDMQCE--SERYHLYRYWARFLCFYKEQPLNLI	263
Qy	336	RRYFGEKVALYFAWL	GFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSK--DSFEM	393
		: ::    :	:   :   :	
Db	264	KKYYGEKIGIYFAWL	GFYTEMLFYAAVMGVICFVYGVLSYEDNITSKEICDPKIGGMIVM	323
Qy	394	CPLC-LDCPFWLLSS	AALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSATLAYRW	452
		:    :   :	:       :  :       :	
Db	324	CPLCDKKCSYWKLN	STCLSSWQSHLFDNEGTVFFAMFMGIWVTLFLEFWKRRQARLEYEW	383
Qy	453	DCSDYEDTEE--RPR	PQFAASAPMTAPNPITGEDEPYFPERSRARRMLAGSVVIVVMVAV	510
		:: : :  ::	:   : :	
Db	384	DLVDFEEEEQQQLQ	IRPEYEQKCTGRRLNRITQEMEPYLPFPSKCARFCLSGATVLFWTCL	443
Qy	511	VVMCLVSIILYR---	AIMAIVVSRSGNTLLAAWASRI-----ASLTGSVVNLVFILILS	561
		:   :: :        :	: :     :        :	
Db	444	IVACIMGVIAYRLA	VYAAFASVMKDSSTSKIQLVGSLITPQLATSVTASCINFVILILN	503
Qy	562	KIYVSLAHVLTRWEM	HRTQTKFEDAFTLKVFIFQFVNFYSSPVYIAFFKGRFVGYPGNYH	621
		:  :  :    :  :::	::   ::	
Db	504	FLYEHVAIWITDMEI	PKTHLEYENKLTMKMFMFQFVNYYSSCFYVAFFKKGKFGVPGNYS	563
Qy	622	TLFG---VRNEECAAG	GCLIELAQELLVIMVGKQVINNMQEVLIPLKLGWWQKFRLRSK	677
		:  :	: ::      :    :  :	
Db	564	YMFGKWSTLRNEEC	APGGCLIELTTQLLIVMAGKQMVGNVQEALLPLVRNWW-----S	616
Qy	678	KRKAGASAGASQGP	WEDDYELVPCE--GLFDEYLEMVLQFGFVTIFVAACPLAPLALLN	735
		: :      ::	:    :	
Db	617	SRKGRSHPESTYSR	WEQDHDLQNFSQLGLFYEYLEMVIQFGFITLFVASFPLAPLLALFN	676

Qy 736 NWVEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISNAFLLAFSSDFLPR-- 793  
| :|:|:| | | :|:|:| :|:| | | : :|:|:|:|:|:| | :| |  
Db 677 NILEVRVDAWKFTTQFRRPMAAKARNIGAWEEILNVVAIMSVVTNAFIMAFTSDMIPRLV 736  
  
Qy 794 ---AYYRWTRAHDLRGFLNFTLA-----RAPSSF AAAHNRTCRYRAFRD 834  
| | : | :| :| :| :| | | :| :| | | :| |  
Db 737 YLYAYHPGIEA-NMTGYITNSLSIYNISQIPEDNLPEAGENPSWFNSSTITTCRYRDYRY 795  
  
Qy 835 DDGH---YSQT--YWNLLAIRLAFVIVFEHVVSFVGRLLDLLVPDIPESVEIKVKREYYL 889  
| | | : | :|:|:| :|:|:| :| | | | : | :|:|:| | : :|:|:| :|  
Db 796 PPGHLRQYTHTMQFWHILAAKLAFAIIIMEHVVFVVKFFVAWLIPDVPSEVKARIKRERFL 855  
  
Qy 890 AKQALAENEV 899  
: : | | |  
Db 856 VQEYHLHNYEV 865

RESULT 11

Q1AP37\_STRPU

ID Q1AP37\_STRPU Unreviewed; 921 AA.  
AC Q1AP37;  
DT 11-JUL-2006, integrated into UniProtKB/TrEMBL.  
DT 11-JUL-2006, sequence version 1.  
DT 24-JUL-2007, entry version 6.  
DE 122 kDa protein TMEM16.  
OS Strongylocentrotus purpuratus (Purple sea urchin).  
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
OC Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;  
OC Strongylocentrotus.  
OX NCBI\_TaxID=7668;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Galindo B.E., Moy G.W., Vacquier V.D.;  
RT "A 122 kDa protein from Strongylocentrotus purpuratus embryo belongs  
RT to TMEM16 protein family."  
RL Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.  
CC -----  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC -----  
DR EMBL; DQ020164; AAY82885.1; -; mRNA.  
DR UniGene; Spu.15325; -.  
DR InterPro; IPR007632; DUF590.  
DR PANTHER; PTHR12308; DUF590; 1.  
DR Pfam; PF04547; DUF590; 1.  
PE 2: Evidence at transcript level;  
SQ SEQUENCE 921 AA; 106699 MW; 9A516A5DCA1ADCCC CRC64;

Query Match 30.2%; Score 1497; DB 2; Length 921;  
Best Local Similarity 38.6%; Pred. No. 2.1e-113;  
Matches 330; Conservative 149; Mismatches 291; Indels 86; Gaps 19;

Qy 102 GSPAK-----PRIADFVLVWEEDLKLDRQQDSAARDRTDMHRTWRETFLDN 147  
| | | | | | | | : | | | : | :|:| | : : : | : | |  
Db 59 GSPAKKDDNKVNDLFFKDGKRRIDFVLAY-----RKQSESEEREKRVKK--RQNFAN 109

Qy	148	LRAAGLCV-----DQQDVQDGNNTTVHYALLSASWAVLCYYAEDLRLKLPLQEL	195
Db	110	LIDEGLQLEYENSEGPEPKEDDPESHGRT--FFVKVHAPWDLMTRYAEELKIKMPIEEN	167
Qy	196	PNQASNWSAGLLAWLGIPNVLLLEVVPDVPPEYYSCRFRVKNLPRFLGSDNQDTFFTSTKR	255
Db	168	NMEEPVNVFNCIDKLWTPFELSEYVKPEPDVFTAPFIRDRASEFI-MESQDTFFPNNIR	226
Qy	256	HQILFEILAKTPYGHEKKNLLGIHQLLAEGVLSAAFPLHDGPFKTP----PEGPQAPRLN	311
Db	227	NRVVYEILERMRYDANDPTKFGIDHLIANGSYFAAYPLHEGDYKSKHSLTHGPQ----N	282
Qy	312	QRQVLFQHWARWGKWNKYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVG	371
Db	283	DRHLLYE EWARSGRWYKKQPLDLIRCYFGEKIGIYFCWLGFYTEMLTWAGFVGLIVFLYG	342
Qy	372	CFLVFSDIPTQELCGSKDSFEMCPLC-LDCPFWLLSSACALAQAGRLFDHGGTVFFSLFM	430
Db	343	CISLPSSVVVQEICAGTDII-MCPLCDKRCPYWTLSDSCFYSKLTYLFDNEATVFFACFM	401
Qy	431	ALWAVLLLEYWKRKSATLAYRWDCSDYEDTEERPRPQFAASAPMTAPNPITGEDEPYFPE	490
Db	402	SLWATMFCEFWKRRQNTIDYDWDLFGFEEQEENIRPEFEAKAPDRRVSPITNLPEQYMKF	461
Qy	491	RSRARRMLAGSVVIVVMVAVVVMCLVSIILYRAIMAIVVSRSGNTLLAAWASRIASLTGS	550
Db	462	SKRFPREFSTSVPTIAFMILLVMAAVMTVIVYRIVVKTAFIDQEFISSYASIITSVTAS	521
Qy	551	VVNLVFILILSKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNIFYSSPVYIAFFK	610
Db	522	MISLILIMILQILYERIAVWLTNLELHRTETETEDSFTFKMYLFAFVNYYSTSFYIAFFK	581
Qy	611	GRFVGYPGNYHTLFGV-RNEECAAGGCLIELAQELLVIMVGKQVINNMQEVLPKLKGWW	669
Db	582	GRLPGTPADYGRVFGIWRQEECDPAGCTQELFINIAITMCGKQFFNNFMELAMPVLMNFW	641
Qy	670	QKFRLRSKKRKAGASAGASQGPWEDDYELVPC--EGLFDEYLEMVLQFGFVTIFVAACPL	727
Db	642	RS-RTGRKEEKSGK---GRYEQWEQDADLADLGPRGLFKEYLEMVVQFGFSTIFVAAFPL	697
Qy	728	APLFALLNNWVEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISNAFLLAFS	787
Db	698	APLFALLNNLVEVRLDAYKFISQLRRPVAKRAQDIGAWYAILVTVGNLVLTNALVIAFT	757
Qy	788	SDFLPR---AYYRWTRAHDLRGFLNFTLA-----RAPSSFAAAHNRT-----	826
Db	758	SEFIPRQVFKYYYYGGPEATLNGYTNSLSYFNTVDMQNDSKPTDPSYPRVGDEDTTDPNY	817
Qy	827	-----CRYRAFRDDDGHYSQT--YWNLLAIRLAFVIVFEHVVSFVGRLLDLLVPDIPES	878
Db	818	GLNVSVCRYRGNYDE--HYNVTLDYWLVIKLAIFILLYEHFVLFTHKFFVAYIIPDMPEF	875
Qy	879	VEIKVKREYYLAKQAL	894
Db	876	VKNOIKRETYLGOQAL	891

## RESULT 12

## TM16A\_MOUSE

ID TM16A\_MOUSE Reviewed; 960 AA.  
 AC Q8BHY3; Q6P5C6; Q8BI26; Q99JK1;  
 DT 29-MAY-2007, integrated into UniProtKB/Swiss-Prot.  
 DT 29-MAY-2007, sequence version 2.  
 DT 24-JUL-2007, entry version 32.  
 DE Transmembrane protein 16A.  
 GN Name=Tmem16a;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muroidea; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).  
 RC STRAIN=C57BL/6J; TISSUE=Head, and Kidney;  
 RX PubMed=16141072; DOI=10.1126/science.1112014;  
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,  
 RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,  
 RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,  
 RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,  
 RA Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,  
 RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,  
 RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,  
 RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,  
 RA di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,  
 RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,  
 RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,  
 RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,  
 RA Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,  
 RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,  
 RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,  
 RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,  
 RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,  
 RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,  
 RA Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,  
 RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,  
 RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,  
 RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,  
 RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,  
 RA Schoenbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,  
 RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,  
 RA Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,  
 RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,  
 RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,  
 RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,  
 RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,  
 RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,  
 RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,  
 RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,  
 RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,  
 RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,

RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,  
 RA Hayashizaki Y.;  
 RT "The transcriptional landscape of the mammalian genome.";  
 RL Science 309:1559-1563(2005).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 2).  
 RC STRAIN=C57BL/6, and Czech II; TISSUE=Eye, and Mammary tumor;  
 RX PubMed=15489334; DOI=10.1101/gr.2596504;  
 RG The MGC Project Team;  
 RT "The status, quality, and expansion of the NIH full-length cDNA  
 RT project: the Mammalian Gene Collection (MGC).";  
 RL Genome Res. 14:2121-2127(2004).  
 CC -!- SUBCELLULAR LOCATION: Cell membrane; Multi-pass membrane protein  
 CC (By similarity). Cytoplasm (By similarity).  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=1;  
 CC IsoId=Q8BHY3-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=Q8BHY3-2; Sequence=VSP\_025672;  
 CC -!- SIMILARITY: Belongs to the TMEM16 family.  
 CC -!- SEQUENCE CAUTION:  
 CC Sequence=BAC35051.1; Type=Miscellaneous discrepancy; Note=Wrong choice of frame;  
 CC -----  
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
 CC Distributed under the Creative Commons Attribution-NoDerivs License  
 CC -----  
 DR EMBL; AK028991; BAC26230.1; ALT\_INIT; mRNA.  
 DR EMBL; AK029329; BAC26398.1; ALT\_INIT; mRNA.  
 DR EMBL; AK052589; BAC35051.1; ALT\_SEQ; mRNA.  
 DR EMBL; BC006062; AAH06062.1; ALT\_INIT; mRNA.  
 DR EMBL; BC062959; AAH62959.1; -; mRNA.  
 DR UniGene; Mm.26700; -.  
 DR Ensembl; ENSMUSG00000031075; Mus musculus.  
 DR MGI; MGI:2142149; Tmem16a.  
 DR ArrayExpress; Q8BHY3; -.  
 DR InterPro; IPR007632; DUF590.  
 DR PANTHER; PTHR12308; DUF590; 1.  
 DR Pfam; PF04547; DUF590; 1.  
 PE 2: Evidence at transcript level;  
 KW Alternative splicing; Cytoplasm; Glycoprotein; Membrane;  
 KW Transmembrane.  
 FT CHAIN 1 960 Transmembrane protein 16A.  
 FT /FTId=PRO\_0000288436.  
 FT TOPO\_DOM 1 333 Cytoplasmic (Potential).  
 FT TRANSMEM 334 354 Potential.  
 FT TOPO\_DOM 355 402 Extracellular (Potential).  
 FT TRANSMEM 403 423 Potential.  
 FT TOPO\_DOM 424 493 Cytoplasmic (Potential).  
 FT TRANSMEM 494 514 Potential.  
 FT TOPO\_DOM 515 539 Extracellular (Potential).  
 FT TRANSMEM 540 560 Potential.  
 FT TOPO\_DOM 561 581 Cytoplasmic (Potential).  
 FT TRANSMEM 582 602 Potential.  
 FT TOPO\_DOM 603 705 Extracellular (Potential).  
 FT TRANSMEM 706 726 Potential.

FT TOPO\_DOM 727 765 Cytoplasmic (Potential).  
 FT TRANSMEM 766 786 Potential.  
 FT TOPO\_DOM 787 856 Extracellular (Potential).  
 FT TRANSMEM 857 877 Potential.  
 FT TOPO\_DOM 878 960 Cytoplasmic (Potential).  
 FT CARBOHYD 806 806 N-linked (GlcNAc. . .) (Potential).  
 FT VAR\_SEQ 448 451 Missing (in isoform 2).  
 FT /FTid=VSP\_025672.  
 SQ SEQUENCE 960 AA; 110916 MW; BFD0112FD310CE88 CRC64;

Query Match 30.1%; Score 1489; DB 1; Length 960;  
 Best Local Similarity 37.5%; Pred. No. 1e-112;  
 Matches 361; Conservative 170; Mismatches 303; Indels 128; Gaps 29;

Qy 26 GLYCRDQAHAERWAMT--SETSSGSHCARSRMLRRRAQEEDSTVLIDVSPPEAEKRGSYG 83  
 ||| || : : : : || || | || : | : | :  
 Db 52 GLYFRDGKRKVDYILVYHHKRASG-----SRTLARRGLQNDMVL-----GTRS 94

Qy 84 STAHASEPGGQQAACRAGSPAKPRIADFLVWEEDLKLDRQQDSAARDRTDMHRTWRET 143  
 || : : |||| | : | : | | ||  
 Db 95 VRQDQPLPG--KGSPVDAGSPEVP-----MDYHEDD-----KRFRREE 130

Qy 144 FLDNLRAAGLCVDQQDVQDGNTTVH---YALLSASWAVLCYYAEDLRLKLPLQELPNQAS 200  
 : || ||| :: | : | : | : | ||| || |::| : : : :  
 Db 131 YEGNLLEAGLELE---NDEDTKIHGVGFKIHAPWHVLCREAEFLKLKMPTKKVYHISE 186

Qy 201 NWSAGLLAWLGIPNVLLEVVPDVPPEYYSCRFRVNKLPRFLGS-----DNQDTFFT 251  
 : ||| | : || :: : | : | : | : : : |||  
 Db 187 --TRGLLK--TINSVLQKITDPIQPKVAEHRPQTTKRLSYPPFSREKQHLFDLTD RDSFFD 242

Qy 252 STKRHQILFEILAKTPYGHEKKNLLGIHQLLAEGVLSAAFPLHDGPFKTPPEGPQAPRLN 311  
 | | |::||| : | : : || ||| || |||:|||| : || |  
 Db 243 SKTRSTIVYEILKRTTCTKAKYS-MGITSLLANGVYSAAYPLHDGDY----EGDNV-EFN 296

Qy 312 QRQVLFQHWARWGKWNKYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVG 371  
 |::|:: || : | : ||||:| ||:||||| ||||| || |::|::|| :||| |  
 Db 297 DRKLLYEEWASYGVFYKYQPIDLVRKYFGEKVGLYFAWLGAYTQMLIPASIVGVIVFLYG 356

Qy 372 CFLVFSDIPTQELCGSKDSFEMCPLC-LDCPFWLLSSACALAQAGRLFDHG GTVFVSLFM 430  
 | | :||: |:| : : |||| | : | :|||| |:| |||: ||||:|  
 Db 357 CATVDENIPSMEMCDQRYNITMCPLCDKTC SYWKMSACATARASHLFDNPATVFFSVFM 416

Qy 431 ALWAVLLLEYWKRKSATLAYRWDCSDYEDTEE----RPRPQFAA----SAPMTAPNPIT 481  
 |||| :|:|||| | |||| : :| || || :: | | : | |  
 Db 417 ALWAATFMEHWKRKQMRNLNRYRWDLTGFEEEEEA VKDHPRAEYEARVLEKSLRKESRNKET 476

Qy 482 GEDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLVSIILYRAIMAIVVSRSGNTLLAAWA 541  
 | : | | | : | : || : : | : || | : : : : : :  
 Db 477 --DKVKLTWRDRFPAYFTNLVSIIFMIAVTFAIVLGVIIYRISTAAALAMNSSPSVRSNI 534

Qy 542 SRIASLTGSVVNLVFILILSKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIQFVNFYS 601  
 : | : :||| |::| :| :| ||: | : :| :| : | | | :||| | :  
 Db 535 RVTVTATAVIINLVVILLDEVYGC IARWLTKIEVPKTEKSFEERLTFKAFLK FVNSYT 594

Qy 602 SPVYIAFFKGRFVGYPGNYHTLF-GVRNEECAAGGCLIELAQELLVIMVGKQVI--NNMQE 659

```

      |:||||| ||:| :| | ||| |||:| :| :||:|:| ||: |
Db      595 PIFYVAFFKGRFVGRPGDYVYIFRSFRMEECAPGGCLMELCIQLSIIMLGKQLIQNNLFE 654

Qy      660 VLIPKLKGWWQKFRLRSKKRKAGASAGASQGPWEDDYELVPCEGLFDEYLEMVLQFGFVT 719
      : |||:| : : :|| : : :| | : | | || :||:|:| |||||
Db      655 IGIPKMKKFIRYLKLRRQSPSDREEYVVRKQRYEVDNFLEPFAGLTPEYMEMIIQFGFVT 714

Qy      720 IFVAACPLAPLFPALLNNWVEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVIS 779
      :|||: ||||| ||||| :|||:| ||| | |||| ||:||||:| || : ||||
Db      715 LFVASFPLAPLFPALLNNIIEIRLDAKKFVTELRRPVAIRAKDIGIWIYNILRGVGKLAVII 774

Qy      780 NAFLLAFSSDFLPRAYYRWTRAHD--LRGFLNFTLARAPSSF-----AAAHN----- 824
      |||:|:|:|:| || | : : : : ||:| || || | |
Db      775 NAFVISFTSDFIPRLVYLYMYSQNGTMHG FVNHTL----SSFNVSDFQNGTAPNDPLDLG 830

Qy      825 ---RTCRYRAFRD---DDGHY--SQTYWNLLAIRLAFVIVFEHVVFVSVGRLLDLLVPDIP 876
      : |||: :|: : | | : :| :|| |||||:|:| : :| :|||
Db      831 YEYQICRYKDYREPPWSEHKYDISKDFWAVLAARLAFVIVFQNLVMFMSDFVDWVIPDIP 890

Qy      877 ESVEIKVKREYYL-----AKQALAENEVLFGTNGTKDEQPKGSELSSHWTPFTVP 926
      : : : :| | || | : : : |:|: :| :| | |
Db      891 KDISQQIHKEKVLMLVELFMREEQGKQQLLDTWM-----EKEKPRDVPCNNH-SPTTHP 942

Qy      927 KA 928
      :|
Db      943 EA 944
```

RESULT 13

TM16A\_HUMAN

```

ID      TM16A_HUMAN                      Reviewed;          986 AA.
AC      Q5XXA6; Q8IYY8; Q8N7V3;
DT      29-MAY-2007, integrated into UniProtKB/Swiss-Prot.
DT      23-NOV-2004, sequence version 1.
DT      21-AUG-2007, entry version 18.
DE      Transmembrane protein 16A (Discovered on gastrointestinal stromal
DE      tumors protein 1) (Oral cancer overexpressed protein 2) (Tumor
DE      amplified and overexpressed sequence 2).
GN      Name=TMEM16A; Synonyms=DOG1, ORAOV2, TAOS2;
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC      Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND TISSUE SPECIFICITY.
RX      PubMed=16906560; DOI=10.1002/gcc.20371;
RA      Huang X., Godfrey T.E., Gooding W.E., McCarty K.S. Jr., Gollin S.M.;
RT      "Comprehensive genome and transcriptome analysis of the 11q13 amplicon
RT      in human oral cancer and synteny to the 7F5 amplicon in murine oral
RT      carcinoma.";
RL      Genes Chromosomes Cancer 45:1058-1069(2006).
RN      [2]
RP      NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 3).
RC      TISSUE=Testis;
RX      PubMed=14702039; DOI=10.1038/ng1285;
```



RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,  
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,  
 RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,  
 RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,  
 RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,  
 RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,  
 RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,  
 RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,  
 RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,  
 RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,  
 RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,  
 RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y.,  
 RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,  
 RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,  
 RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,  
 RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,  
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,  
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,  
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,  
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,  
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,  
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,  
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,  
 RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,  
 RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,  
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,  
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,  
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;  
 RT "Complete sequencing and characterization of 21,243 full-length human  
 RT cDNAs.";  
 RL Nat. Genet. 36:40-45(2004).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 2).  
 RC TISSUE=Testis;  
 RX PubMed=15489334; DOI=10.1101/gr.2596504;  
 RG The MGC Project Team;  
 RT "The status, quality, and expansion of the NIH full-length cDNA  
 RT project: the Mammalian Gene Collection (MGC).";  
 RL Genome Res. 14:2121-2127(2004).  
 RN [4]  
 RP IDENTIFICATION, AND TOPOLOGY.  
 RX PubMed=12739008;  
 RA Katoh M., Katoh M.;  
 RT "FLJ10261 gene, located within the CCND1-EMS1 locus on human  
 RT chromosome 11q13, encodes the eight-transmembrane protein homologous  
 RT to C12orf3, C11orf25 and FLJ34272 gene products.";  
 RL Int. J. Oncol. 22:1375-1381(2003).  
 RN [5]  
 RP SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.  
 RX PubMed=15215166;  
 RA West R.B., Corless C.L., Chen X., Rubin B.P., Subramanian S.,  
 RA Montgomery K., Zhu S., Ball C.A., Nielsen T.O., Patel R.,  
 RA Goldblum J.R., Brown P.O., Heinrich M.C., van de Rijn M.;  
 RT "The novel marker, DOG1, is expressed ubiquitously in gastrointestinal  
 RT stromal tumors irrespective of KIT or PDGFRA mutation status.";

RL Am. J. Pathol. 165:107-113(2004).  
 RN [6]  
 RP SUBCELLULAR LOCATION.  
 RX PubMed=16261155; DOI=10.1038/sj.onc.1209203;  
 RA Carles A., Millon R., Cromer A., Ganguli G., Lemaire F., Young J.,  
 RA Wasylyk C., Muller D., Schultz I., Rabouel Y., Dembele D., Zhao C.,  
 RA Marchal P., Ducray C., Bracco L., Abecassis J., Poch O., Wasylyk B.;  
 RT "Head and neck squamous cell carcinoma transcriptome analysis by  
 RT comprehensive validated differential display."  
 RL Oncogene 25:1821-1831(2006).  
 CC -!- SUBCELLULAR LOCATION: Cell membrane; Multi-pass membrane protein.  
 CC Cytoplasm.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=3;  
 CC Name=1;  
 CC IsoId=Q5XXA6-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=Q5XXA6-2; Sequence=VSP\_025665, VSP\_025668, VSP\_025669;  
 CC Note=No experimental confirmation available;  
 CC Name=3;  
 CC IsoId=Q5XXA6-3; Sequence=VSP\_025666, VSP\_025667, VSP\_025668,  
 CC VSP\_025669, VSP\_025670, VSP\_025671;  
 CC Note=No experimental confirmation available;  
 CC -!- TISSUE SPECIFICITY: Broadly expressed with higher levels in liver  
 CC and skeletal muscle.  
 CC -!- SIMILARITY: Belongs to the TMEM16 family.  
 CC -----  
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
 CC Distributed under the Creative Commons Attribution-NoDerivs License  
 CC -----  
 DR EMBL; AY728143; AAU82085.1; -; mRNA.  
 DR EMBL; AK097619; BAC05123.1; -; mRNA.  
 DR EMBL; BC033036; AAH33036.2; -; mRNA.  
 DR UniGene; Hs.503074; -.  
 DR Ensembl; ENSG00000131620; Homo sapiens.  
 DR HGNC; HGNC:21625; TMEM16A.  
 DR MIM; 610108; gene.  
 DR PharmGKB; PA128394678; -.  
 DR ArrayExpress; Q5XXA6; -.  
 DR InterPro; IPR007632; DUF590.  
 DR PANTHER; PTHR12308; DUF590; 2.  
 DR Pfam; PF04547; DUF590; 1.  
 PE 1: Evidence at protein level;  
 KW Alternative splicing; Cytoplasm; Glycoprotein; Membrane; Polymorphism;  
 KW Transmembrane.  
 FT CHAIN 1 986 Transmembrane protein 16A.  
 FT /FTId=PRO\_0000288435.  
 FT TOPO\_DOM 1 333 Cytoplasmic (Potential).  
 FT TRANSMEM 334 354 Potential.  
 FT TOPO\_DOM 355 402 Extracellular (Potential).  
 FT TRANSMEM 403 423 Potential.  
 FT TOPO\_DOM 424 519 Cytoplasmic (Potential).  
 FT TRANSMEM 520 540 Potential.  
 FT TOPO\_DOM 541 565 Extracellular (Potential).  
 FT TRANSMEM 566 586 Potential.  
 FT TOPO\_DOM 587 606 Cytoplasmic (Potential).

FT	TRANSMEM	607	627	Potential.
FT	TOPO_DOM	628	731	Extracellular (Potential).
FT	TRANSMEM	732	752	Potential.
FT	TOPO_DOM	753	791	Cytoplasmic (Potential).
FT	TRANSMEM	792	812	Potential.
FT	TOPO_DOM	813	882	Extracellular (Potential).
FT	TRANSMEM	883	903	Potential.
FT	TOPO_DOM	904	986	Cytoplasmic (Potential).
FT	CARBOHYD	832	832	N-linked (GlcNAc. . .) (Potential).
FT	VAR_SEQ	1	116	Missing (in isoform 2).
FT				/FTId=VSP_025665.
FT	VAR_SEQ	1	28	Missing (in isoform 3).
FT				/FTId=VSP_025666.
FT	VAR_SEQ	29	36	GYLPSEGT -> MLTRPSQV (in isoform 3).
FT				/FTId=VSP_025667.
FT	VAR_SEQ	448	451	Missing (in isoform 2 and isoform 3).
FT				/FTId=VSP_025668.
FT	VAR_SEQ	476	501	Missing (in isoform 2 and isoform 3).
FT				/FTId=VSP_025669.
FT	VAR_SEQ	651	700	CAPGGCLMELCIQLSIIMLGKQLIQNNLFEIGIPKMKKLIR
FT				YLKLKQQSP -> VTEILFISGSPFCLAYDLSTPCTWEKQL
FT				QHICSAKSSRFLSFLLETFLFP (in isoform 3).
FT				/FTId=VSP_025670.
FT	VAR_SEQ	701	986	Missing (in isoform 3).
FT				/FTId=VSP_025671.
FT	VARIANT	608	608	F -> S (in dbSNP:rs2186797).
FT				/FTId=VAR_032417.
FT	VARIANT	983	983	G -> R (in dbSNP:rs3740722).
FT				/FTId=VAR_032418.
FT	CONFLICT	801	801	N -> D (in Ref. 3; AAH33036).
FT	CONFLICT	948	948	W -> C (in Ref. 3; AAH33036).
SQ	SEQUENCE	986 AA;	114078 MW;	E30A02F91EF36FC2 CRC64;

Query Match 29.9%; Score 1482; DB 1; Length 986;  
Best Local Similarity 36.8%; Pred. No. 4e-112;  
Matches 365; Conservative 162; Mismatches 302; Indels 164; Gaps 30;

Qy	26	GLYCRDQAHAERWAMT--SETSSGSHCARSRLRRRAQEEDSTVLIDVSPPEAEKRGSYG	83
		: : :    :          :	
Db	52	GLYFRDGRRKVDYILVYHHKRPSG-----NRTLVRVQHS DTP-----SGA	92
Qy	84	STAHASEPGGQQAACRAGSPAKPRIADFLVWEEDLKLDRQQDSAARDRTDMHRTWRET	143
		:   :  :       :  :	
Db	93	RSVKQDHPLPGKGASLDAGSGEPP-----MDYHEDD-----KRFRREE	130
Qy	144	FLDNLRAAGLCVDQQDVQDGNTTVH--YALLSASWAVLCYYAEDLRLKLPLQELPNQAS	200
		:        :: :  :  :  : :            :  :  :: : :	
Db	131	YEGNLLLEAGLELE---RDEDTKIHGVGFVKIHAPWNVLCREAEFLKLKMPTKKMYH--I	184
Qy	201	NWSAGLLAWLGIPNVLLEVVPDPPEYYSCR-----FRVNKLPRFLGSDNQDTFF	250
		:       :   :: :  :             : :	
Db	185	NETRGLLK--KINSVLQKITDPIQPKVAEHRPQTMKRLSYFPSREKQHLFDLSD-KDSFF	241
Qy	251	TSTKRHQILFEILAKTPYGHEKKNLLGIHQLLAEGVLSAAFPLHDGPFKTPPEGPQAPRL	310
		::    :    : :          :  :     : :	

Db	242	DSKTRSTIVYEILKRTTCTKAKYS-MGITSLLANGVYAAAYPLHDGDY-----NGENVEF	295
Qy	311	NQRQVLFQHWARWGKWNKYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLV	370
		:: ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::	
Db	296	NDRKLLYE EWARYGVFYKYQPIDLVRKYFGEKIGLYFAWLGVYTQMLIPASIVGIIVFLY	355
Qy	371	GCFLVFSDIPTQELCGSKDSFEMCPLC-LDCPFWLLSSACALAQAGRLFDHGGTVFFSLF	429
		: : :: ::  : :  ::   ::   ::   ::   ::   ::   ::   ::	
Db	356	GCATMDENIPSMEMCDQRHNTMCPLCDKTC SYWKMSACATARASHLFDNPATVFFSVF	415
Qy	430	MALWAVLLLEYWKRKSATLAYRWDCSDYEDTEE----RPRPQFAA-----SAPMTAPNPI	480
		::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::	
Db	416	MALWAATFMEHWKRKQMRNLNYRWDLTGFE EEEEEAVKDHPRAEYEARVLEKSLKKESRKN-	474
Qy	481	TGEDEPYFPERS-----RARRMLAG-----SVVIVVMVAVVVM	513
		:       : :	
Db	475	--EKRRHIPEESTNKWKQRVKTAMAGVKLTDKVKLTWRDRFPAYLTNLVSIIFMIAVTFA	532
Qy	514	CLVSIILYRAIMAIIVVSRSGNTLLAAWASRIASLTGSVNVLVFILILSKIYVSLAHVLTR	573
		:: : ::      :: : : : : : : :   : ::   ::   ::   ::   ::	
Db	533	IVLGVIIRISMAAALAMNSSPSVRSNIRVTVTATAVIINLVVIILLDEVYGCARWLTK	592
Qy	574	WEMHRTQTKFEDAFTLKVFIFQFVN FYSSPVYIAFFKGRFVGYPGNYHTLF-GVRNEECA	632
		: : ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::	
Db	593	IEVPKTEKSFEERLIFKAFL LKFVNSYTIPIFYVAFFKGRFVGRPGDYVYIFRSFRMEECA	652
Qy	633	AGGCLIELAQELLVIMVGKQVI-NNMQEVLIPKLKGWWQKFRLRSKKRKAGASAGASQGP	691
		::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::	
Db	653	PGGCLMELCIQLSIIMLGKQLIQNNLFEIGIPKMKKLIRYLKLKQQSPPDHEECVKRKQR	712
Qy	692	WEDDYELVPCEGLFDEYLEMVLQFGFVTIFVAACPLAPLFALLNNWVEIRLDARKFVCEY	751
		:	
Db	713	YVDYNLEPFAGLTPEYMEMIIQFGFVTLFVASFPLAPLFALLNNIIEIRLDAKKFVTEL	772
Qy	752	RRPVAERAQDIGIWFHILAGLTHLAVISNAFLLAFSSDFLPRA--YYRWTRAHDLRGFLN	809
		::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::	
Db	773	RRPVAVRAKDIGIWINILRGIGKLAVIINAFVISFTSDFIPRLVYLYMYSKNGTMHGFPVN	832
Qy	810	FTLARAPSSF-----AAAHN-----RTCRYRAFRD---DDGHY--SQTYWNLLA	848
Db	833	HTL----SSFNVSD FQNGTAPNDPLDLGYEVQICRYKDYREPPWSENKYDISKDFWAVLA	888
Qy	849	IRLAFVIVFEHVVF SVGRLLDLLVPDIPESVEIKVKREYYLA-----KQALAENE	898
Db	889	ARLAFVIVFQNLVMFMSDFVDWVIPDIPKDISQQIHKEKVL MVELFMREEQDKQQLL--E	946
Qy	899	VLFGTNGTKDEQP-----KGSELSSH	919
Db	947	TWMEKERQKDEPPCNHNTKACPD SLGSPAPSH	979

RESULT 14  
Q8CFW1\_MOUSE  
ID Q8CFW1\_MOUSE Unreviewed; 913 AA.  
AC Q8CFW1;  
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.

DT 01-MAR-2003, sequence version 1.  
 DT 24-JUL-2007, entry version 21.  
 DE Transmembrane protein 16B.  
 GN Name=Tmem16b;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muroidea; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Eye;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Eye;  
 RG NIH MGC Project;  
 RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.  
 CC -----  
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
 CC Distributed under the Creative Commons Attribution-NoDerivs License  
 CC -----  
 DR EMBL; BC033409; AAH33409.1; -; mRNA.  
 DR UniGene; Mm.333398; -.  
 DR Ensembl; ENSMUSG00000038115; Mus musculus.  
 DR MGI; MGI:2387214; Tmem16b.  
 DR GO; GO:0016021; C:integral to membrane; IEA:UniProtKB-KW.  
 DR InterPro; IPR007632; DUF590.  
 DR PANTHER; PTHR12308; DUF590; 1.  
 DR Pfam; PF04547; DUF590; 1.  
 PE 2: Evidence at transcript level;  
 KW Transmembrane.  
 SQ SEQUENCE 913 AA; 104388 MW; CA17DB27D8167F64 CRC64;

Query Match 29.6%; Score 1467.5; DB 2; Length 913;

Best Local Similarity 38.1%; Pred. No. 5.6e-111;  
Matches 331; Conservative 167; Mismatches 274; Indels 97; Gaps 22;

Qy	78	KRGS---YGSTAH--ASEPGGQQAACRAGSPAKPRIADFLVWEEDLKLDRQQDSAARD	132
		: :       :     :	
Db	20	KRGAHLGHGSPGHSLAVISNGETGKERHGGGPGDVELGPLDALEEE-----	65
Qy	133	RTDMHRTWRETFLDNLRAAGLCVDQQDVQDGNTTVHYALLSASWAVLCYYAEDLRLKLPL	192
		:         : : : : : : :             : : :	
Db	66	----RREQRDEFENLMAAGLEL-EKDLESKSQGSVFVRIHAPWQVLAREAEFLKIKVPT	120
Qy	193	QEL-----PNQASNWSAGLLAWLGIPNVLLEVVPDVPPEYYSCRFRVNLKP-----RF	240
		: : : : :   :   :     :     : :   :	
Db	121	KKMYEIKAGGSIKAKFSA-ILQTLSSP-----LQPRV-PEHSNNRMKNLSYPFSREKMYL	173
Qy	241	LGSDNQDTFFTSTKRHQILFEILAKTPYGHEKKNLLGIHQLLAEGVLSAAFFPLHDGPFT	300
		:       :   : :     :   :     :   :       : :	
Db	174	YNIQEKDTFFDNATRSRIVHEILKRTACS-RANNTMGINSLIANNIYEAAYPLHDGEYDS	232
Qy	301	PPEGPQAPRLNQRQVLFQHWARWGKWNKYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPA	360
		: : :     : :     : :     : :     : :     : :	
Db	233	PGDD-----MNDRKLLYQEWARYGVFYKFQPIDLRKYFGEKIGLYFAWLGLYTSFLIPS	287
Qy	361	AVVGTLLVFLVGCFLVFSDIPTQELCGSKDSFEMCPLC-LDCPFWLLSSACALAQAGRLFD	419
		:   :   :       :     : : :   :           :	
Db	288	SVIGVIVFLYGCATIEEDIPSKEMCDHQNAFTMCPLCDKSCDYWNLSSACGTARASHLFD	347
Qy	420	HGGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCSDYEDTEER----PRPQF-----	468
		:         :         :         :   :         : :	
Db	348	NPATVFFSIFMALWATMFLENWKRLQMR LGYFWDLTGIEEEEEERSQEHSRPEYETKVREK	407
Qy	469	-----AASAPMTAPNPITGE-DEPYFPERSRARRMLAGSVVIVVMVAVVMCLVSIIL	520
		:   :   :       :     :   :   : : : :	
Db	408	LLKESGKSAVQKLEANSPEDEDEDKLTWKDRFPGYLMNFASILFMIALTFSIVFGVIV	467
Qy	521	YRAIMAIVVSRSGNTLLAAWASRI--ASLTGSVVNLVFILILSKIYVSLAHVLRWEMH	577
		:       : :   :         :   :   :	
Db	468	YRITTAAALS-----LNKATRSNVRVTVTATAVIINLVVILILDEIYGAVAKWLTKEVP	522
Qy	578	RTQTKFEDAFTLKVFIFQFVN FYSSPVYIAFFKGRFVGYPGNYHTLF-GVRNEECAAGGC	636
		:   :   :     : :     :             :   :	
Db	523	KTEQTFEERLILKAFL LKFVNAYSPIFYVAFFKGRFVGRPGSYVYVFDGYRMEECAPGGC	582
Qy	637	LIELAQELLVIMVGKQVI--NNMQEVLIPKLKGWWQKFRRLRSKKRKAGASAGASQGPWEDD	695
		:   :   :     :   :   :   : : : : : :   :	
Db	583	LMELCIQLSIIMLGKQLIQNNIFEIGVPKLKKLFRKLKDETEPGESDPDHSKRPEQWDLD	642
Qy	696	YELVPCEGLFDEYLEMVLQFGFVTIFVAACPLAPL FALLNNWVEIRLDARKFVCEYRRPV	755
		:         :   : :     :     :     :     :	
Db	643	HSLEPYTGLTPEYMEMIIQFGFVTLFVASFPLAPVFALLNNVIEVRLDAKKFVTELRRPD	702
Qy	756	AERAQDIGIWFHILAGLTHLAVISNAFLLA FSSDFLPRAYRWTRAHD--LRGFLNFTLA	813
		:           :   : :     :     :     :	
Db	703	AVRTKDIGIWF DILSGIGKFSVIINAFVIAVTSDFIPRLVYQYSYSHNGTLHG FVNHTLS	762
Qy	814	-----RAPSSFAAAHNRTC RYRAFRD-----DDGHYSQTYWNLLAIRLAFVIVF	857

```

      :  :|      : ||:: :|:      :  :|: ||::|: |||||:|
Db      763 FFNVSQLKEGTQPENSQFDQEVQFCRFKDYREPPWAPNPYEFQYWSVLSARLAFVIF 822

Qy      858 EHVVFSSVGRLLDLLVPDIPESVEIKVKRE 886
      :::| : |::| ::||| : :::|
Db      823 QNLVMFLSVLVDWMIPDIPTDISDQIKKE 851
```

RESULT 15

TM16B\_HUMAN

```
ID      TM16B_HUMAN                      Reviewed;          999 AA.
AC      Q9NQ90;
DT      16-JAN-2004, integrated into UniProtKB/Swiss-Prot.
DT      01-OCT-2000, sequence version 1.
DT      24-JUL-2007, entry version 35.
DE      Transmembrane protein 16B.
GN      Name=TMEM16B; Synonyms=C12orf3;
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC      Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      NUCLEOTIDE SEQUENCE [MRNA].
RC      TISSUE=Retina;
RA      Lorenz B., White K.E., Econs M.J., Strom T.M.;
RT      "Transcripts in 12p13.3.";
RL      Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
CC      -!- SUBCELLULAR LOCATION: Membrane; Multi-pass membrane protein
CC      (Probable).
CC      -!- SIMILARITY: Belongs to the TMEM16 family.
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NoDerivs License
CC      -----
DR      EMBL; AJ272204; CAC01125.1; -; mRNA.
DR      UniGene; Hs.148970; -.
DR      Ensembl; ENSG00000047617; Homo sapiens.
DR      KEGG; hsa:57101; -.
DR      HGNC; HGNC:1183; TMEM16B.
DR      MIM; 610109; gene.
DR      PharmGKB; PA25504; -.
DR      LinkHub; Q9NQ90; -.
DR      ArrayExpress; Q9NQ90; -.
DR      GermOnline; ENSG00000047617; Homo sapiens.
DR      InterPro; IPR007632; DUF590.
DR      PANTHER; PTHR12308; DUF590; 1.
DR      Pfam; PF04547; DUF590; 1.
PE      2: Evidence at transcript level;
KW      Membrane; Polymorphism; Transmembrane.
FT      CHAIN           1           999           Transmembrane protein 16B.
FT                                     /FTId=PRO_0000072564.
FT      TRANSMEM       360       382           Potential.
FT      TRANSMEM       535       557           Potential.
FT      TRANSMEM       577       599           Potential.
```

Query Match 29.6%; Score 1464; DB 1; Length 999;  
Best Local Similarity 37.4%; Pred. No. 1.2e-110;  
Matches 344; Conservative 167; Mismatches 284; Indels 124; Gaps 27;

Qy	80	GSYGSTAHASEPGGQQAAACRAGSPAKPRIADFVLVWEEDLKLDROQDSAADRTDMHRT	139
		::   : :  :	
Db	125	GETGKEPHAGGPG-----DIELG-PLDALEEERKEQ---	154
Qy	140	WRETFLDNLRAAGLCVDQQDVQDGNTTVHYALLSASWAVLCYYAEDLRCLKPLQELPNQ-	198
		: :: ::: : : :            :: :  : : :	
Db	155	-REEFEHNLM EAGLEL-EKDLENKSQGSIFVRIHAPWQVLAREAEFLKIKVPTKKEMYEI	212
Qy	199	-----ASNWSAGLLAWLGIPNVLLEVVPDPPEYYSCRFRVNKLKLP-----RFLGSDNQ	246
		:     : :        : : : :   : :	
Db	213	KAGGSIAKKFSAAL-----QKLSSHLQPRV-P EHSNNKMKNLSYPFSREKMYLYNIQE K	265
Qy	247	DFTFFTSTKRHQILFEILAKTPYGHEKKNLGLIHQLLAEGVLSAAFPLHDGPFKTPPEGPQ	306
		:   : :     :    :  :  :  :   :      : :  :	
Db	266	DTFFDNATRSRIVHEILKRTACS-RANNTMGINSLIANNIYEAYPLHDGEYDSPEDD--	322
Qy	307	APRLNQRQVLFQHWA RWGKW NKYQPLDHVRRYFG EKVALYFAWLGFYTGWLLPA AVVGTL	366
		:   :: :     :  :  : :  : :      :       : : :: :  :	
Db	323	--MNDRKLLYQEWARYGVFYKFQPIDLRKYFGEKIGLYFAWLGLYTSFLIPSSVIGVI	379
Qy	367	VFLVGCFLVFSDIPTQELCGSKDSFEMCPLC-LDCPFWLLSSACALAQAGRLF DHGGTVF	425
		:    :: :  ::         :              :	
Db	380	VFLYGCATIEEDIPSREMCDQQNAFTMCPLCDKSCDYWNLSSACGTAQASHLFDNPATVF	439
Qy	426	FSLFMALWAVLLLEYWK RK SATLAYRWDCSDYEDTEER----PRPQFAA-----	470
		:      :               :  :       ::	
Db	440	FSIFMALWATMFLENWKRLQMRLGYFWDLTGIEEEEEERAQEHSRPEYETKVREKMLKESN	499
Qy	471	-SAPMTAPNPIT----GEDEPYFPERSRAR RMLAGSVVIVVMVAVVVMCLVSIILYRAIM	525
		:   :      :  : : : : :	
Db	500	QSAVQKLETNTTECGDEDDEDKLTWKDRFPGYLMNFASILFMIALTFSIVFGVIVYRITT	559
Qy	526	AIVVSRSNGNTLLAAWASRI---ASLTGSVVNLVFILILSKIYVSLAHVLTRWEMHRTQTK	582
		:        : :   :         :  :    :  : : :	
Db	560	AAALS-----LNKATRSNVRVTVTATAVIINLVVILILDEIYGAVAKWLTKIEVPKTEQT	614
Qy	583	FEDAFTLKVFIFQFVN FYSSPVYIAFFKGRFVGYPGN YHTLF-GVRNEECAAGGCLIELA	641
		:     : :        :          :  :              :	
Db	615	FEERLILKAFL LKFVNAYSPIFYVAFFKGRFVG RPSYVYVFDGYRMEECAPGGCLMELC	674
Qy	642	QELLVIMVGKQVI-NNMQEVLIPKLKGWWQKFRLRSKKRKAGASAGA-SQGP--WEDDYE	697
		:  :  :         :  : :    :    : :   :    :    :	



Db	675	IQLSIIMLGKQLIQNNIFEIGVPKLK---KLFRKLKDETEAGETDSAHSKHPEQWDLDYS	731
Qy	698	LVPCEGLFDEYLEMVLQFGFVTIFVAACPLAPLFALLNWNVEIRLDARKFVCEYRRPVAE	757
		: :: :     : ::     :     : :    :	
Db	732	LEPYTGLTPEYMEMIIQFGFVTLFVASFPLAPVFALLNNVIEVRDLAKKFVTELRRPDVAV	791
Qy	758	RAQDIGIWFHILAGLTHLAVISNAFLLAFFSSDFLPAYYYRWTRAHD--LRGFLNFTLA--	813
		:          ::  :       ::  :    :     :::  :     :    :	
Db	792	RTKDIGHWFDILSGIGKFSVISNAFVIAITSDFIPLRVYQYSYSHNGTLHG FVNHTLSFF	851
Qy	814	-----RAPSSF AAAHNRTCRYRAF RD-----DDGHYSQTYWNLLAIRLAFVIVFEH	859
		: :  :   ::  : : :  :  :    :  :       : ::	
Db	852	NVSQ LKEGTQPENSQFDQE VQFCRF KDYREPPWAPNPYEFSKQYW FILSARLAFVI IFQN	911
Qy	860	VVFSVGRLDLLVPDI P ESVEIKVKRE-----YYLAKQALAENEVLFGTNGTKDEQPKG	913
		:  :  :  ::    : :::  :::  :  :    :	
Db	912	LVMFLSVLV DWMIPDIPTDISD QIKKEKS LLVDFFLKE----EHEKLKLMDEPALRSPGG	967
Qy	914	SELSSHWPFTVPKA-SQL	931
		:   :	
Db	968	GDRSR SRAASSAPSGQSQL	986

Search completed: June 24, 2008, 08:41:08  
Job time : 524 secs

2023